

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw mode]

Run on: November 26, 2005, 00:09:54 ; Search time 10 Seconds (without alignments)

104.265 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAAPKONTWYAGG..... DRRVIEVKGKYEVVTTQPG 344

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

RESULT 1
US-10-058-730-227

; Sequence 227, Application US/10858730

; Publication No. US2005055568A1

; GENERAL INFORMATION:

; APPLICANT: Bailey, Richard B.

; APPLICANT: Blomquist, Paul

; APPLICANT: Doten, Reed

; APPLICANT: Driggers, Edward M.

; APPLICANT: Madden, Kevin T.

; APPLICANT: O'Leary, Jessica

; APPLICANT: O'Toole, George

; APPLICANT: Trueheart, Joshua

; APPLICANT: Walbridge, Michael J.

; APPLICANT: Yorgov, Peter S.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID

; TITLE OF INVENTION: PRODUCTION

; FILE REFERENCE: 14184-030001

; CURRENT APPLICATION NUMBER: US/10/858,730

; CURRENT FILING DATE: 2004-05-01

; PRIORITY APPLICATION NUMBER: US 60/475,000

; PRIORITY FILING DATE: 2003-05-30

; PRIORITY APPLICATION NUMBER: US 60/551,860

; NUMBER OF SEQ ID NOS: 364

; SEQ ID NO: 227

; SOFTWARE: FastSEQ for Windows Version 4.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	5.2	417	1 US-10-058-730-227	Sequence 227, App
2	93	5.1	229	1 US-10-510-386-228	Sequence 228, App
3	93	5.1	410	1 US-10-793-626-3258	Sequence 3258, App
4	93	5.1	477	1 US-10-793-626-3250	Sequence 3250, App
5	84	4.6	1992	7 US-11-013-759-3	Sequence 3, App1
6	84	4.6	1992	7 US-11-013-759-13	Sequence 13, App1
7	84	4.6	2047	7 US-11-013-759-4	Sequence 4, App1
8	84	4.6	2047	7 US-11-013-759-7	Sequence 4, App1
9	84	4.6	2053	7 US-11-013-759-9	Sequence 9, App1
10	83.5	4.6	585	1 US-10-510-386-20	Sequence 20, App1
11	83.5	4.6	594	1 US-10-510-386-38	Sequence 18, App1
12	83.5	4.6	721	7 US-11-060-920-5	Sequence 5, App1
13	81.5	4.5	543	1 US-10-495-664-3	Sequence 3, App1
14	81	4.5	348	1 US-10-793-626-2866	Sequence 2866, App
15	79	4.3	334	1 US-10-802-796-128	Sequence 728, App
16	79	4.3	444	7 US-11-074-176-170	Sequence 170, App
17	78	4.3	259	1 US-10-510-386-108	Sequence 108, App
18	76.5	4.2	251	7 US-11-054-515-1833	Sequence 1833, App
19	75	4.1	249	7 US-11-054-515-1753	Sequence 1753, App
20	75	4.1	524	7 US-11-082-389-10	Sequence 10, App1
21	73	4.0	1213	7 US-11-074-176-256	Sequence 256, App
22	72.5	4.0	643	1 US-10-510-386-8	Sequence 8, App1
23	72	3.9	227	1 US-10-858-730-86	Sequence 86, App1
24	72	3.9	635	1 US-10-501-039-84	Sequence 4, App1
25	71.5	3.9	579	1 US-10-821-234-1352	Sequence 949, App

ALIGNMENTS

RESULT 1
US-10-058-730-227

; Sequence 227, Application US/10858730

; Publication No. US2005055568A1

; GENERAL INFORMATION:

; APPLICANT: Bailey, Richard B.

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; APPLICANT: O'Toole, George

; APPLICANT: Trueheart, Joshua

; APPLICANT: Walbridge, Michael J.

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID

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; FILE REFERENCE: 14184-030001

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; CURRENT FILING DATE: 2004-05-01

; PRIORITY APPLICATION NUMBER: US 60/475,000

; PRIORITY FILING DATE: 2003-05-30

; PRIORITY APPLICATION NUMBER: US 60/551,860

; NUMBER OF SEQ ID NOS: 364

; SEQ ID NO: 227

; LENGTH: 417

; TYPE: PRT

; ORGANISM: Escherichia coli

; US-10-058-730-227

Qy 59 VNPYLGPFMGYDWLGRMAYKGSVNDGAFKAQGVQLAKGYPTDLDIYTRLGGMVWRA 118

Db 93 VQPHSGSQANFVAYTALLPEGDTVLGNLAHGHLTH--GSPVNFSGLYNI--VPGI 147

Qy 119 DSKG--NYASTEVSRSHD---TGSPVFGQGVWAVTRDIATRL-BYQWNINIDGAGT 171

Db 148 DATGHDYADLEKQAREHKPKMILIGFSAYSGVVDWAKMREADSIGAYLFVDMAHAGL 207

Qy 172 VTRPNDGMLSLGVSVRFQGQDAAPVYAPAPAPAEV--ATGHTFTKSDVLFNFKATLK 229

Db 208 V-----AAGVYPNPVPHAHVVTTHKTLAG----- 233

Query Match 5.1%; Score 93.5; DB 1; Length 229;
 Best Local Similarity 26.8%; Pred. No. 0.092; Mismatches 22; Indels 51; Gaps 4;
 Matches 33; Conservative 22; Mismatches 51; Indels 17; Gaps 4;

Query 215 LKSDVLLFNPKATLKPPEGQDALDOLYTQLSNMPKDGSAAVVLGYDRIGSEAY--NQQ 270
 Database 116 LQEAVLFDGSKADLKDQAHPLHKAIVLKSV--SNPIRVECHTDSRPISTYRFPSNWE 172

Query 271 LSEKRAQSYVVDLYAK-GIPAGKTSARGMGESENPTVTGNTCDNTVKARALIDCLAPDRVE 329
 Database 173 LSARASTVIGYFTSKEKLDSSRFRLAIGYADTPKVRDRNTES -----HMKENRVE 223

Query 330 IEV 332
 Database 224 IVI 226

RESULT 3
 US-10-793-626-3258
 Sequence 3258. Application US/107931626
 Publication No. US20050255478A1
 GENERAL INFORMATION:
 APPLICANT: KIMMELRY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: PUS4800S
 CURRENT FILING DATE: 2004-03-04
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 3258
 LENGTH: 410
 TYPE: PRT
 ORGANISM: *Bacillus licheniformis*
 US-10-510-386-228

Query Match 5.1%; Score 93.5; DB 1; Length 229;
 Best Local Similarity 26.8%; Pred. No. 0.092; Mismatches 22; Indels 51; Gaps 4;
 Matches 33; Conservative 22; Mismatches 51; Indels 17; Gaps 4;

Query 215 LKSDVLLFNPKATLKPPEGQDALDOLYTQLSNMPKDGSAAVVLGYDRIGSEAY--NQQ 270
 Database 116 LQEAVLFDGSKADLKDQAHPLHKAIVLKSV--SNPIRVECHTDSRPISTYRFPSNWE 172

Query 271 LSEKRAQSYVVDLYAK-GIPAGKTSARGMGESENPTVTGNTCDNTVKARALIDCLAPDRVE 329
 Database 173 LSARASTVIGYFTSKEKLDSSRFRLAIGYADTPKVRDRNTES -----HMKENRVE 223

Query 330 IEV 332
 Database 224 IVI 226

RESULT 4
 US-10-793-626-3250
 Sequence 3250. Application US/10793626
 Publication No. US20050255478A1
 GENERAL INFORMATION:
 APPLICANT: KIMMELRY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: PUS4801S
 CURRENT APPLICATION NUMBER: US/10/793, 626
 CURRENT FILING DATE: 2004-10-04
 PRIOR APPLICATION NUMBER: US/10/793, 626
 PRIOR FILING DATE: 2004-03-04
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3250
 LENGTH: 477
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: amino acid sequence

Query Match 5.1%; Score 93; DB 1; Length 477;
 Best Local Similarity 20.1%; Pred. No. 0.27; Mismatches 116; Indels 124; Gaps 20;
 Matches 74; Conservative 48; Mismatches 116; Indels 124; Gaps 20;

Query 12 KDNNTWAGKLGKGSQYHDTGFYGNNGFQNNNGPTRNDGAGAFGGQVNPYLGFGNG-- 68
 Database 75 KDNNGKNTYTK-AQGKCTEFYKNNNSNTLG-----YNGNLLGPTKLKCGDKV 122

Query 69 -----YDWLGRMAYKGSYDNG-----AFKAGQVQLTAKGY---- 99
 Database 123 KIKLINNLDENTTFHWIG-LEVNGKDGPSQVIKPGKEKTIKFENQDSATLWYHPPS 181

Query 100 PITDDDIYTRIGGMWYRADS-KGNVASTGVSRSEHDGTGUSPVFAGGVEAVTRD--IA 155
 Database 182 PNTAK-QVYNGLGLVYIEDSKRNLP-----SDYGRNDLP-----IQDKTKEV 226

Query 156 TRLEYQVNNGI DAGTVG-TRPDNGMISLGGSYRFQEDAAVPAVAPAPAPEVATKHF 214
 Database 227 KKLNSYKTKD--EDGTQGDTVLVNG1VN-----PKLTKEEK 261

Query 215 LKSDVLL-FNFNPKATLKPPEGQDALDLYT--QLS-----NMPDPRGSAYVLGYTDR 261
 Database 262 IRLRLNGSNARDLNKLNSRNSPEVIAASDQGLKNAKKRLKEINLRSERKEIVIDLSKM 321

Query 262 IGSE-----AYNQOLSEKRAQSYVVDLYAKGKTSARGMGESENPTVTGNT 308
 Database 322 KGEKISLVNDKTVLPIISNKERKSSNRGNTP--KVSK----KIKLEGMDNDVTINGNK 373

Query 309 CD 310
 Database 374 FD 375

Qy 215 LKSDVIL--FNFNKATLKPEQGQQLDQLYT--QLS-----NMDPKDGSAVVLGYTDR 261
 Db 262 IRLRLNGNARDNLKLSSNNQSFETYIASDGGQKNAKRLKEINLAPSERKEIVIDLKSM 321
 Qy 262 1GSE-----AYNQOLSEKRAQSVDVYLVAKG1PAGKISARGMGBSNPVTGNT 308
 Db 322 KGERKISLVDNDKTVLPIKNSKEKSNKGNTP--KVSK-----KIKLEGMMNDVTINGNK 373
 Qy 309 CD 310
 Db 374 FD 375

RESULT 5

us-013-759-3

Sequence 3, Application US/11013759
 Publication No. US20050249747A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Sasaki, Ken
 APPLICANT: Yang, Yan Ping
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
 FILE REFERENCE: 1038-921MIS:1b
 CURRENT APPLICATION NUMBER: US/11/013,759
 CURRENT FILING DATE: 2004-12-16
 PRIORITY APPLICATION NUMBER: US/09/361,619
 PRIORITY FILING DATE: 1999-07-27
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 13
 LENGTH: 1992
 TYPE: PRT
 ORGANISM: Moraxella catarrhialis
 US-11-013-759-13

Query Match 4.6%; Score 84; DB 7; Length 1992;
 Best Local Similarity 20.1%; Pred. No. 11; Gaps 17;
 Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;

Qy 18 AGGRGLGNSQYHDGTFYNGQFQNNGPTRNDQLGAGA----FGGYQVNFPYLG----PEM 67
 Db 959 SGLKAGKSTLNDGGL----S1KNPPTGSEQ1QVAGDGVKFAKVNNGVVGAGIDGTRI 1012
 Qy 68 GYDWLGRMAYKGSYDNG-----AFKAQGVQLT-AKLGYPITDDLDIYTRI/GMMVWR-- 117
 Db 1013 TRDEIGFTGTGNSLDKSKPHLSKRDGNGAGKKTINQSGEIAQNSHDAVT--GGKLYDLK 1070
 Qy 118 -----ADSKGNYASTGVNNIGDAGTGTRPDMGMSLGVSYRFGOEDAAPVAPAPAPEVATKHF 214
 Db 1071 TELEKISSSTAKTAQNSLHEFSVADEQCNMFTVSNPYSSYDT-----SKTSVD 1157
 Qy 155 ATRLEYQWVNNIGDAGTGTRPDMGMSLGVSYRFGOEDAAPVAPAPAPEVATKHF 214
 Db 1119 IT-----FAGENG-ITTKVNGVVRGIIQTKG-----LTTPLLTVGNNN 1157
 Qy 18 AGGRGLGNSQYHDGTFYNGQFQNNGPTRNDQLGAGA----FGGYQVNFPYLG----PEM 67
 Db 959 SGLKAGKSTLNDGGL----S1KNPPTGSEQ1QVAGDGVKFAKVNNGVVGAGIDGTRI 1012
 Qy 68 GYDWLGRMAYKGSYDNG-----AFKAQGVQLT-AKLGYPITDDLDIYTRI/GMMVWR-- 117
 Db 1013 TRDEIGFTGTGNSLDKSKPHLSKRDGNGAGKKTINQSGEIAQNSHDAVT--GGKLYDLK 1070
 Qy 118 -----ADSKGNYASTGVNNIGDAGTGTRPDMGMSLGVSYRFGOEDAAPVAPAPAPEVATKHF 214
 Db 1071 TELEKISSSTAKTAQNSLHEFSVADEQCNMFTVSNPYSSYDT-----SKTSVD 1118
 Qy 155 ATRLEYQWVNNIGDAGTGTRPDMGMSLGVSYRFGOEDAAPVAPAPAPEVATKHF 214
 Db 1119 IT-----FAGENG-ITTKVNGVVRGIIQTKG-----LTTPLLTVGNNN 1157
 Qy 215 LKSDVLFNFNKATLKPEQGQQLDQLYTQNSMDPKDGSAVVLGYTDRIGSEAYNQOLSEK 274
 Db 1158 GK2IVDSQN-----GQNTTIGLSNLANTNDKGSVRITBQGNTIKDE----DKT 1204
 Qy 275 RAQSVVDVYLVAKG1PAGKISARGMGS-----NPVTGNTC-----DNVKARAA 317
 Db 1205 RAASIVDVLSA-----GFLNQGNGAEVDVSTYDTNFADEGNATTAKVYDDTSKTSKV 1258
 Qy 318 LIDCLAPDRRVIEVK--GYKEVVTQDAG 344
 Db 1259 VTDVNVDDTTIEVKDKKLGVKTTTLLSTG 1287

RESULT 7

us-11-013-759-4

Sequence 4, Application US/11013759
 Publication No. US20050249747A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Sasaki, Ken
 APPLICANT: Yang, Yan Ping
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
 FILE REFERENCE: 1038-921MIS:1b
 CURRENT APPLICATION NUMBER: US/11/013,759
 CURRENT FILING DATE: 2004-12-16
 PRIORITY APPLICATION NUMBER: US/09/361,619
 PRIORITY FILING DATE: 1999-07-27
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1

RESULT 6

us-11-013-759-13

Seq ID No 4	Db	1068 TRDEIGFTGTNGSLDKSKRPHLSKDGINAGGKKTINQSEIAONSHDAVT - - - - - GCKIYDLK 1125
LENGTH: 2047	Qy	118 - - - - - ADSKCNYASTGVSRSEHDGTGSPVFAAGVWEAVTRD1 154
TYPE: PRT	Db	1126 TELENKISSTAKTAQNSLHEFSVADEQNNFTVSNPVSSYDT - - - - - SKTSVD 1173
ORGANISM: Moraxella catarrhalis	US-11-013-759-4	
Query Match Score 4.6%; Score 84; DB 7; Length 2047;	Qy	155 ATRLLEYQVNNTIGDAGTVTRPDNGMLSLGVSYRFGQDAAPVAPAPAPEVATKHT 214
Best Local Similarity 20.1%; Prod. No. 11; Mismatches 47; Indels 122; Gaps 17;	Db	1174 IT - - - - - FASENG - - - - - SKNPTSEQVQAGDVKVTRPDNGMLSLGVSYRFGQDAAPVAPAPAPEVATKHT 212
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;	Qy	18 AGKLGKGSQYHDTGFGYNGFQNNGPTRNQLGAGA - - - - - FGGYQVNPNYLG - - - - - FEM 67
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1014 SGLKAGKSTLNDGGL - - - - - SKNPTSEQVQAGDVKVTRPDNGMLSLGVSYRFGQDAAPVAPAPAPEVATKHT 212
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	68 GYDWLGRMAYKGSYDNG - - - - - AFKAQGVQLT-AKLGYPTRDLDIYTRUGGMVVR - - - - - FEM 67
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1068 TRDEIGFTGTNGSLDKSKRPHLSKDGINAGGKKTINQSEIAONSHDAVT - - - - - GCKIYDLK 1125
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	118 - - - - - ADSKCNYASTGVSRSEHDGTGSPVFAAGVWEAVTRD1 154
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1126 TELENKISSTAKTAQNSLHEFSVADEQNNFTVSNPVSSYDT - - - - - SKTSVD 1173
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	155 ATRLLEYQVNNTIGDAGTVTRPDNGMLSLGVSYRFGQDAAPVAPAPAPEVATKHT 214
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1174 IT - - - - - FASENG - - - - - SKNPTSEQVQAGDVKVTRPDNGMLSLGVSYRFGQDAAPVAPAPAPEVATKHT 212
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	215 LKSDVLFNFKATLKPEQQLDOLYTOQNMDPKDGSAVVUGYTRIGSEAYNQQLSEK 274
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1213 GKGIVDQN - - - - - QNTTGLSNTLNQVNTNDKGSVRTTEQGNNIKDE - - - - - DKT 1259
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	275 RAQSVVDYLVAKGIPAGKISARGMGE - - - - - NPVTGNCT - - - - - DNVKARAA 317
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1260 RAASIVDVLSA - - - - - GFNLQNGEAVDFVSTYDVTNFADGNATTAKVYDTSKTSKV 1313
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Qy	318 LIDCLAPDRRVELEVK - - - - - GYKEVVTOPAG 344
Matches 18; Conservative 11; Mismatches 142; Indels 122; Gaps 17;	Db	1314 VYDVNVDDTTIEVRDKKLGVKRTTLTSTG 1342
RESULT 8		
US-11-013-759-9		
Sequence 9, Application US/11013759		
; Publication No. US20050249747A1		
; GENERAL INFORMATION:		
; APPLICANT: Loosmore, Sheena M.		
; APPLICANT: Sasaki, Ken		
; APPLICANT: Yang, Yan Ping		
; APPLICANT: Klein, Michel H.		
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT PROTEIN OF MORAXELLA		
; FILE REFERENCE: 1038-921MIS:jb		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; CURRENT FILING DATE: 2004-12-16		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; TYPE: PRT		
; ORGANISM: Moraxella catarrhalis		
US-11-013-759-9		
Query Match Score 4.6%; Score 84; DB 7; Length 2053;		
Best Local Similarity 20.4%; Prod. No. 11; Mismatches 133; Indels 120; Gaps 17;		
Matches 76; Conservative 43; Mismatches 133; Indels 120; Gaps 17;		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/09/361,619		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 2004-12-16		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2047		
; TYPE: PRT		
; ORGANISM: Moraxella catarrhalis		
US-11-013-759-7		
Query Match Score 4.6%; Score 84; DB 7; Length 2047;		
Best Local Similarity 20.1%; Prod. No. 11; Mismatches 142; Indels 122; Gaps 17;		
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;		
; SEQ ID NO: 9		
; LENGTH: 2047		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2047		
; TYPE: PRT		
; ORGANISM: Moraxella catarrhalis		
US-11-013-759-4		
Query Match Score 4.6%; Score 84; DB 7; Length 2047;		
Best Local Similarity 20.1%; Prod. No. 11; Mismatches 142; Indels 122; Gaps 17;		
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;		
; SEQ ID NO: 9		
; LENGTH: 2047		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2047		
; TYPE: PRT		
; ORGANISM: Moraxella catarrhalis		
US-11-013-759-3		
Query Match Score 4.6%; Score 84; DB 7; Length 2053;		
Best Local Similarity 20.1%; Prod. No. 11; Mismatches 142; Indels 122; Gaps 17;		
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
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; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
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; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
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; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
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; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
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; PRIORITY APPLICATION NUMBER: US/09/361,619		
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; SOFTWARE: Patentin Ver. 2.1		
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; PRIORITY FILING DATE: 1999-07-27		
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; SOFTWARE: Patentin Ver. 2.1		
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; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
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; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		
; PRIORITY FILING DATE: 1999-07-27		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: Patentin Ver. 2.1		
; SEQ ID NO: 9		
; LENGTH: 2053		
; CURRENT APPLICATION NUMBER: US/11/013,759		
; PRIORITY APPLICATION NUMBER: US/09/361,619		

Db 1280 GFNLQGNGRAVDVFYSTDDVNFANGNTTAKVYDDTSKTSKVYDVNVDTTIEVKDKK 1339
 Qy 334 -GYKVVVTOPAG 344
 Db 1340 LGVKTTLTSTG 1351

RESULT 10
 US-10-510-386-20
 Sequence 20, Application US/10510386
 Publication No. US20050244922A1
 GENERAL INFORMATION:
 APPLICANT: Andersen, Jens Toerne
 APPLICANT: Clausen, Ib Groth
 APPLICANT: Jorgensen, Steen Troels
 APPLICANT: Olesen, Peter Bjarke
 APPLICANT: Rasmussen, Michael Dolberg
 TITLE OF INVENTION: Improved Bacillus Host Cell
 FILE REFERENCE: 10294.204-US
 CURRENT APPLICATION NUMBER: US/10/510,386
 CURRENT FILING DATE: 2004-10-04
 NUMBER OF SEQ ID NOS: 288
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 20
 LENGTH: 585
 TYPE: PRT
 ORGANISM: *Bacillus licheniformis*
 US-10-510-386-20

Query Match 4.6%; Score 83.5; DB 1; Length 585;
 Best Local Similarity 26.1%; Pred. No. 2.4;
 Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;

Qy 98 GYITDDDIYTRLGGMWRAKSGKNTAATGVSRSENDTGVSPVAFGVEVAVTRDIATR 157
 Db 382 GYVLDREGWGRL-NLFSAADGYGAF-----TKNVTMDSAKGCFH--TAD-- 426
 Qy 158 LEQWQVNNGDAGTV-----GTRPDNGMISLGVSYRFGQDAA--PV 197
 Db 427 --RWRNDISGTRKLTKGKGALKLEGNTYSGGTRIDQGTLEGGSETAFGRGDAVNGG 483
 Qy 198 VAPAPAP-----APEVATKHTFLKSDVLNFNFKATLKPEQGQALDQLYTOLSN 245
 Db 484 ILKEDAPGKLIIEGDKYKOSAKGILELQLSKDKLQKKGKARLK--GTURLN--FT--DN 537

Qy 246 MDPKDGSAVVLGVTDRIGS 264
 Db 538 YVPADGSAIT-FRKHGS 555

RESULT 11
 US-10-510-386-38
 Sequence 3, Application US/10510386
 Publication No. US20050244922A1
 GENERAL INFORMATION:
 APPLICANT: Andersen, Jens Toerne
 APPLICANT: Clausen, Ib Groth
 APPLICANT: Jorgensen, Steen Troels
 APPLICANT: Olesen, Peter Bjarke
 APPLICANT: Rasmussen, Michael Dolberg
 TITLE OF INVENTION: Improved Bacillus Host Cell
 FILE REFERENCE: 10294.204-US
 CURRENT APPLICATION NUMBER: US/10/510,386
 CURRENT FILING DATE: 2004-10-04
 NUMBER OF SEQ ID NOS: 248
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 38
 LENGTH: 594
 TYPE: PRT
 ORGANISM: *Bacillus licheniformis*
 US-10-510-386-38

Query Match 4.6%; Score 83.5; DB 1; Length 594;

Best Local Similarity 26.1%; Pred. No. 2.4;
 Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;
 Qy 98 GYITDDDIYTRLGGMWRAKSGKNTAATGVSRSENDTGVSPVAFGVEVAVTRDIATR 157
 Db 387 GYVLDREGWGRL-NLFSAADGYGAF-----TKNVTMDSAKGCFH--TAD-- 431
 Qy 158 LEQWQVNNGDAGTV-----GTRPDNGMISLGVSYRFGQDAA--PV 197
 Db 432 --RWRNDISGTRKLTKGKGALKLEGNTYSGGTRIDQGTLEGGSETAFGRGDAVNGG 488
 Qy 198 VAPAPAP-----APEVATKHTFLKSDVLNFNFKATLKPEQGQALDQLYTOLSN 245
 Db 489 ILKEDAPGKLIIEGDKYKOSAKGILELQLSKDKLQKKGKARLK--GTURLN--FT--DN 542

RESULT 12
 US-11-060-920-5
 Sequence 5, Application US/11060920
 Publication No. US20050244378A1
 GENERAL INFORMATION:
 APPLICANT: Kaufman, Paul L
 APPLICANT: Liu, Xuyang
 TITLE OF INVENTION: Method for Treating Glaucoma
 FILE REFERENCE: 960296-00149
 CURRENT APPLICATION NUMBER: US/11/060,920
 CURRENT FILING DATE: 2005-02-18
 PRIOR APPLICATION NUMBER: US 60/545,723
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 5
 LENGTH: 721
 TYPE: PRT
 ORGANISM: *Clostridium botulinum*
 US-11-060-920-5

Query Match 4.6%; Score 83.5; DB 7; Length 721;
 Best Local Similarity 20.9%; Pred. No. 3.1;
 Matches 71; Conservative 39; Mismatches 117; Indels 113; Gaps 17;

Qy 2 KAIFLVNAAPONTWAGKGLGMQSYHDTGFYG-----NGF-QNNNGPFRNDOLGAG 52
 Db 165 KSKFIPN-----NTLFSNAKLNANARDTDRGIPDWEWEINSYVMNQKAVAWDDKFAAN 219
 Qy 53 AFGGYQN-----PYLGBEMGKDWLGRNAYKGSVDN-----GAFKAQGVQ 92
 Db 220 GYKKVSNPFEKCTANPDYTFE-----KVSGOIDPSVSMVARDPMISAYPIVGVQ 270
 Qy 93 --LTAKLGYPTDDIYTRLGGMWRAKSGK-NYASTGVSRSEHDGVSPVAFGGVW 148
 Db 271 MERLUVVSKSETITGDS-----KSMSKSTSNTVGAEVSGSLQAGGIP 320
 Qy 149 AVTRDIATRLEYQWNNNGDAGTVGTRPDNGM-LSIGVS-----VRFQGQEDAAPVYAPA 201
 Db 321 VFSMSAANSHWTQNTSTVDDTTGBFSQQLSINTGESAYINPNTRYNTGAPVYNTV 380
 Qy 202 PAPAPEVATKHTFLKSDVLNFNFKATLKPEQGQAL-----D 237
 Db 381 PT-----TIVIDQSVATK--GOBSLIGDYLNGGTVPIIGERPMALNTMD 426
 Qy 238 QL-----YTQLSNMDPKDGSAYVVLGVTDRIGSEA-YN 268
 Db 427 QFSSRLIPINYNQLSID--NGTVMLISTSQFTGNFAKYN 464

RESULT 13
 US-10-495-664-3
 Sequence 3, Application US/10495664

Publication No. US2005024416A1
 APPLICANT: JING, GUNDRAM
 TITLE OF INVENTION: BISPECIFIC ANTI-CD38 ANTIBODY MOLECULE
 FILE REFERENCE: 03458-0801
 CURRENT APPLICATION NUMBER: US10/495,664
 CURRENT FILING DATE: 2004-05-12
 PRIOR APPLICATION NUMBER: PCT/EP02/12545
 PRIOR FILING DATE: 2002-11-09
 PRIOR FILING DATE: 2001-11-12
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO: 3
 LENGTH: 543
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: protein construct
 US-10-495-664-3

Query Match 4.4%; Score 81; DB 1; Length 348;
 Best Local Similarity 20.9%; Pred. No. 2; Mismatches 90; Indels 160; Gaps 22;
 Matches 77; Conservative 41; Mismatches 75; Indels 12; Gaps 68;

Qy 12 KDNNTWAGGKGWMSQYHDTGFYGNQFONNNGPTRNIDOLGAGAFGGYQVNPNYLGFGMC 6.8
 Db 75 KDNNGKNTLK-AOGKTEPKNNFSNTLG-----YNGLLGPTRLKCKSDKV 122

Qy 69 -----YDWLGRMAYKGSDNG-----AFKAQGVQLTAKGY---- 99
 Db 123 KIRKLINNLDENTFHNG-LEYNGKVDGGPSQVIKPGKEKTIKEFVNQDSATIWHPHPS 181

Qy 100 PITDDLDIYTRLGGMWRAIDS_KGNIASTGVSRSEHDGTGVSPVFAGGVWAVTRD--IA 155
 Db 182 PNTAK-OVNGLISGLLTYEDSKNNP-----SDGKNDLPI-----IJDQDTFVS 226

Qy 156 TRLEYQVNINNIGDAGTYG-TRDNGMILSLGVSYRFQGQDAAPVVAAPAPAPEVATKHF 214
 Db 227 KKLNYSKTKD--EDGTTGDTVLVNGTVN-----PKLTKEK 261

Qy 215 LKSDVLFNPKATLKPQGQALDQLTQLSNTMDPKDGSAVVLYGTYRIGSEAYNQOLSEK 274
 Db 262 IRLRLI-----NGSNARD-LINLKLNSN-----NQSF---- 285

Qy 275 RAQSVDYLVAKGIPAKI-SARGMGESENPNVTGNTCDNVKARAALIDCLAPDRRVEI--- 330
 Db 286 -----RYIASDG---GQLKNAKKLKLKEIN-----LAPSERKEIVID 317

Qy 331 --EVKGYK 336
 Db 318 LSKMKGEK 325

RESULT 15
 US-10-802-796-728
 Sequence 728, Application US/10802796
 Publication No. US20050250104A1
 GENERAL INFORMATION:
 / APPLICANT: COLE, STEWART
 / APPLICANT: BUCHREISER-BROSCH, ROLAND
 / APPLICANT: GORDON, STEPHEN
 / APPLICANT: BILLAULT, ALAIN
 / TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
 / TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC BASED
 / TITLE OF INVENTION: DNA LIBRARY, APPLICATION TO THE DETECTION OF
 / TITLE OF INVENTION: MYCOBACTERIA.
 / FILE REFERENCE: 05394_0011-00000
 / CURRENT APPLICATION NUMBER: US/10/802-796
 / PRIORITY FILING DATE: 2004-03-18
 / PRIORITY APPLICATION NUMBER: US/09/673-476
 / PRIORITY FILING DATE: 2002-03-29
 / PRIORITY APPLICATION NUMBER: PCT/1999/00740
 / PRIORITY FILING DATE: 1999-04-16
 / PRIORITY APPLICATION NUMBER: 09/060,756
 / NUMBER OF SEQ ID NOS: 743
 / SOFTWARE: PatentIn Ver. 2.2
 / SEQ ID NO: 728
 / LENGTH: 334
 / TYPE: PRT
 / ORGANISM: Mycobacterium sp.
 US-10-802-796-728

Query Match 4.3%; Score 79; DB 1; Length 334;
 Best Local Similarity 26.0%; Pred. No. 2.8; Mismatches 56; Indels 58; Gaps 8;
 Matches 44; Conservative 11; Mismatches 11; Indels 11; Gaps 11;

Qy 18 AGGKGWMSQYHDTGFY-GNGFONNNGPTRNIDOLGAGAFGGYQVNPNYLGFGMC-YDNLGRM 75
 Db 187 AGGAGG-----GJUGDGAGGNGLLSSGGAGSFGGGTAGGIVGAGGNAGNAGJFG 240

Qy 76 A-----YKGSDVNGAFAKGQVLTAKGYPITDDLYTRLGGMVNRADSIGNYASTGVS 130
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: amino acid sequence
 US-10-793-626-2866

Sequence 2866, Application US/10793626
 Publication No. US20050255478A1
 GENERAL INFORMATION:
 / APPLICANT: KIMMELLY, WILLIAM JOHN
 / TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 / FILE REFERENCE: PCT/4800S
 / CURRENT APPLICATION NUMBER: US10/793,626
 / CURRENT FILING DATE: 2004-03-04
 / PRIOR APPLICATION NUMBER: 60/164,258
 / PRIOR FILING DATE: 1999-11-09
 / NUMBER OF SEQ ID NOS: 4472
 / SEQ ID NO: 2866
 / LENGTH: 348
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: synthetic
 / OTHER INFORMATION: amino acid sequence
 US-10-793-626-2866

Search completed: November 26, 2005, 00:21:22
Job time : 11 secs

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GenCore version 5.1.6

OM protein - protein search, using SW mode!

Run on: November 26, 2005, 00:10:34 ; Search time 162 Seconds (without alignments)

887.243 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVNLNAPKONTWYAGG.....DRRVEIEVKGYKEVTTQPG 344

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1867565 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/_ptodata/1/_pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/_ptodata/1/_pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/_ptodata/1/_pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/_ptodata/1/_pubpaa/US10_PUBCOMB.pep:*

5: /cgn2_6/_ptodata/1/_pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/_ptodata/1/_pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1823	100.0	344	4	US-10-169-953-2	Sequence 2; Appli
2	1511	82.9	346	4	US-10-467-421-90	Sequence 90; Appli
3	1511	82.9	346	4	US-10-467-421-91	Sequence 97; Appli
4	1511	82.9	346	5	US-10-946-647-1413	Sequence 1413; Appli
5	1511	82.9	346	5	US-10-946-647-1448	Sequence 1448; Appli
6	1505	82.6	346	5	US-10-946-647-1424	Sequence 1424; Appli
7	1499	82.2	350	5	US-10-946-647-1377	Sequence 1377; Appli
8	1495	82.0	350	5	US-10-946-647-1389	Sequence 1389; Appli
9	1495	82.0	350	5	US-10-946-647-1395	Sequence 1395; Appli
10	1495	82.0	350	5	US-10-946-647-1404	Sequence 1404; Appli
11	754	41.4	190	4	US-10-416-708A-24	Sequence 24; Appli
12	754	41.4	192	4	US-10-416-708A-27	Sequence 27; Appli
13	748	41.0	194	4	US-10-416-708A-10	Sequence 10; Appli
14	748	41.0	194	4	US-10-416-708A-64	Sequence 64; Appli
15	719.5	39.5	161	5	US-10-946-647-1436	Sequence 1436; Appli
16	689	37.8	344	4	US-10-336-840-9	Sequence 9; Appli
17	688	37.7	344	4	US-10-336-840-6	Sequence 6; Appli
18	687	37.7	137	4	US-10-412-056-2	Sequence 2; Appli
19	687	37.7	153	3	US-09-905-176-22	Sequence 1; Appli
20	685	37.6	344	4	US-10-336-840-3	Sequence 3; Appli
21	684	37.5	344	4	US-10-316-840-1	Sequence 1; Appli
22	684	37.5	344	4	US-10-316-840-2	Sequence 2; Appli
23	684	37.5	344	4	US-10-336-840-4	Sequence 4; Appli
24	684	37.5	344	4	US-10-316-840-7	Sequence 7; Appli
25	684	37.5	344	4	US-10-336-840-10	Sequence 10; Appli
26	689.5	37.3	341	4	US-10-336-840-5	Sequence 5; Appli
27	680.5	37.3	341	4	US-10-336-840-8	Sequence 8; Appli

ALIGNMENTS

RESULT 1

US-10-169-953-2

; Sequence 2, Application US-10169953

; Publication No. US20030044915A1

; GENERAL INFORMATION:

; APPLICANT: Thierry BAUSSANT

; APPLICANT: Pascal JEANNIN

; APPLICANT: Yves DELNESTE

; APPLICANT: Francois LANNY

; APPLICANT: Jean-Yves BONNEFOY

; TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT

; TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT

; FILE REFERENCE: D18390

CURRENT APPLICATION NUMBER: US/10/169,953

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: FR 00 000700

PRIOR FILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

; LENGTH: 344

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; FEATURE: P40

US-10-169-953-2

Query Match 100.0%; Score 1823; DB 4; Length 344;

Best Local Similarity 100.0%; Pred. No. 1 3e-160;

Matches 344; Conservative 0; Missmatches 0; Gaps 0;

Qy 1 MKAIFVNLNAPKONTWYAGGKLGWSOYHDTGKYGNQFQNNNGPTRNDLGAGAFGGTQVN 60

Db 1 MKAIFVNLNAPKONTWYAGGKLGWSOYHDTGKYGNQFQNNNGPTRNDLGAGAFGGTQVN 60

Qy 1 MKAIFVNLNAPKONTWYAGGKLGWSOYHDTGKYGNQFQNNNGPTRNDLGAGAFGGTQVN 60

Db 1 MKAIFVNLNAPKONTWYAGGKLGWSOYHDTGKYGNQFQNNNGPTRNDLGAGAFGGTQVN 60

Qy 61 PYLGFEMGYDWLGRMAYKGSVNDNGAKAQGVQLTAKLGQYPTDDLDYTRLCGMWVRADS 120

Db 61 PYLGFEMGYDWLGRMAYKGSVNDNGAKAQGVQLTAKLGQYPTDDLDYTRLCGMWVRADS 120

Qy 61 KGNYASTGVSRSEBDTGSPVFAAGVWATRDIATRLEYQVNNGDAGTVTRPDNGM 180

Db 61 KGNYASTGVSRSEBDTGSPVFAAGVWATRDIATRLEYQVNNGDAGTVTRPDNGM 180

Qy 181 LSLGVSYRFQGQDAAPVAP 240

Db 181 LSLGVSYRFQGQDAAPVAP 240

Qy 121 KGNYASTGVSRSEBDTGSPVFAAGVWATRDIATRLEYQVNNGDAGTVTRPDNGM 180

Db 121 KGNYASTGVSRSEBDTGSPVFAAGVWATRDIATRLEYQVNNGDAGTVTRPDNGM 180

Page 2

RESULT 2		RESULT 3	
Qy	301 SNPVTGNTCDNVKARAALIDCLAPDRRVETEVKGYKEVVTOPAG 344	US-10-467-421-90	US-10-467-421-97
Db	301 SNPVTGNTCDNVKARAALIDCLAPDRRVETEVKGYKEVVTOPAG 344	; Sequence 90, Application US/10467421	; Sequence 97, Application US/10467421
	; Publication No. US20040116665A1	; Publication No. US20040116665A1	; Publication No. US20040116665A1
	; GENERAL INFORMATION:		; GENERAL INFORMATION:
	; APPLICANT: Berthet, Francois-Xavier Jacques		; APPLICANT: Berthet, Francois-Xavier Jacques
	; APPLICANT: Denoel, Philippe		; APPLICANT: Denoel, Philippe
	; APPLICANT: Neyt, Cecile Anne		; APPLICANT: Neyt, Cecile Anne
	; APPLICANT: Poolman, Jan		; APPLICANT: Poolman, Jan
	; APPLICANT: Thonnard, Joelle		; APPLICANT: Thonnard, Joelle
	; TITLE OF INVENTION: Vaccine Composition		; TITLE OF INVENTION: Vaccine Composition
	; FILE REFERENCE: B45759		; FILE REFERENCE: B45759
	; CURRENT APPLICATION NUMBER: US/10/467,422		; CURRENT APPLICATION NUMBER: US/10/467,422
	; CURRENT FILING DATE: 2003-08-08		; CURRENT FILING DATE: 2003-08-08
	; PRIOR APPLICATION NUMBER: PCT/EP02/01361		; PRIOR APPLICATION NUMBER: PCT/EP02/01361
	; PRIOR FILING DATE: 2002-02-08		; PRIOR FILING DATE: 2002-02-08
	; PRIOR APPLICATION NUMBER: GB 0103171.5		; PRIOR APPLICATION NUMBER: GB 0103171.5
	; NUMBER OF SEQ ID NOS: 98		; NUMBER OF SEQ ID NOS: 98
	; SOFTWARE: FastSEQ for Windows Version 4.0		; SOFTWARE: FastSEQ for Windows Version 4.0
	; SEQ ID NO 90		; SEQ ID NO 90
	; LENGTH: 346		; LENGTH: 346
	; TYPE: PRT		; TYPE: PRT
	; ORGANISM: E. coli		; ORGANISM: E. coli
	; US-10-467-421-90		; US-10-467-421-90
Qy	82.9%; Score 151; DB 4; Length 34	82.9%; Score 151; DB 4; Length 34	82.9%; Score 151; DB 4; Length 34
Db	Best Local Similarity 84.9%; Pred. No. 1.3e-131; Mismatches 286; Conservative 17; Mismatches 24; Indels 8	Best Local Similarity 84.9%; Pred. No. 1.3e-131; Mismatches 286; Conservative 17; Mismatches 24; Indels 8	Best Local Similarity 84.9%; Pred. No. 1.3e-131; Mismatches 286; Conservative 17; Mismatches 24; Indels 8
Qy	6 VLNAAPKDNTWYAGKGLGMWSQYHDTGFGNNGFQNNNGPTRNQDQLGAGAF	6 VLNAAPKDNTWYAGKGLGMWSQYHDTGFGNNGFQNNNGPTRNQDQLGAGAF	6 VLNAAPKDNTWYAGKGLGMWSQYHDTGFGNNGFQNNNGPTRNQDQLGAGAF
Db	18 VAGAAPKDNNTWYTCAKLGMWSQYHDTGFGF1----NNNGPTHENQLGAGAF	18 VAGAAPKDNNTWYTCAKLGMWSQYHDTGFGF1----NNNGPTHENQLGAGAF	18 VAGAAPKDNNTWYTCAKLGMWSQYHDTGFGF1----NNNGPTHENQLGAGAF
Qy	66 ENGYDWLGRMAYAKGSVDNGAPKAQCVQLTAKLGYPITDDIYTRGGMM	66 ENGYDWLGRMAYAKGSVDNGAPKAQCVQLTAKLGYPITDDIYTRGGMM	66 ENGYDWLGRMAYAKGSVDNGAPKAQCVQLTAKLGYPITDDIYTRGGMM
Db	73 EMGYDWLGRMGSVNGAYKAQCVQLTAKLGYPITDDIYTRGGMM	73 EMGYDWLGRMGSVNGAYKAQCVQLTAKLGYPITDDIYTRGGMM	73 EMGYDWLGRMGSVNGAYKAQCVQLTAKLGYPITDDIYTRGGMM
Qy	126 STGVSRSRSEHDGTGSPVFAAGGVEAWTRDIASTRLEYQWNNGDAGTGTG	126 STGVSRSRSEHDGTGSPVFAAGGVEAWTRDIASTRLEYQWNNGDAGTGTG	126 STGVSRSRSEHDGTGSPVFAAGGVEAWTRDIASTRLEYQWNNGDAGTGTG
Db	131 --VYKNDHTGSPVFAAGGVEATPEIASTRLEYQWNNGDAHTGTT	131 --VYKNDHTGSPVFAAGGVEATPEIASTRLEYQWNNGDAHTGTT	131 --VYKNDHTGSPVFAAGGVEATPEIASTRLEYQWNNGDAHTGTT
Qy	186 SYRFGQEDAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	186 SYRFGQEDAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	186 SYRFGQEDAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP
Db	188 SYRFGQGEAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	188 SYRFGQGEAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	188 SYRFGQGEAAPVYAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP
Qy	246 MDPDRGSAYVVLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS	246 MDPDRGSAYVVLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS	246 MDPDRGSAYVVLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS
Db	248 LPDKDGSUVVGLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS	248 LPDKDGSUVVGLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS	248 LPDKDGSUVVGLGYTDRIGSEAYNQOLSEKRAQSYYVDYLVARGIIPAKSIS
Qy	306 GNTCDNYKARAALIDCLAPDRRVETEVKGYKEVVTOPAG 342	306 GNTCDNYKARAALIDCLAPDRRVETEVKGYKEVVTOPAG 342	306 GNTCDNYKARAALIDCLAPDRRVETEVKGYKEVVTOPAG 342
Db	308 GNTCDNYKQRAALIDCLAPDRRVETEVKGYKEVVTOPAG 344	308 GNTCDNYKQRAALIDCLAPDRRVETEVKGYKEVVTOPAG 344	308 GNTCDNYKQRAALIDCLAPDRRVETEVKGYKEVVTOPAG 344
	; TITLE OF INVENTION: Vaccine Composition	; TITLE OF INVENTION: Vaccine Composition	; TITLE OF INVENTION: Vaccine Composition
	; FILE PREFERENCE: B45759		; FILE PREFERENCE: B45759

1	CURRENT APPLICATION NUMBER:	US 10/467,421
1	CURRENT FILING DATE:	2003-08-08
1	PRIOR FILING DATE:	PCT/EP02/01361
1	PRIOR APPLICATION NUMBER:	GB 0103171.5
1	PRIOR FILING DATE:	2002-02-08
1	NUMBER OF SEQ ID NOS:	98
1	SOFTWARE:	FastSEQ for Windows Version 4.0
1	SEQ ID NO:	97
1	LENGTH:	34 6
1	TYPE:	prt
1	ORGANISM:	E.coli
1	US-10-467-421-97	
1	Query Match	82.9% ; Score 1511;
1	Best Local Similarity	84.9% ; Pred. No. 1;
1	Matches 286; Conservative 17; Mismatch 1	
Qy	6 VLNAAPKDNTWYAGGKLGWSQYHDGFGYGNCG	
Db	18 VAGRAPKDNTWGTGAKLGWSQYHDGTFI----	
Qy	66 EMGYDWLMGRMAYKGSVNDNGASKAQGVOLTAK	
Db	73 EMGYDWLMGRMAYKGSVNGAYKAQGQVLTAK	
Qy	126 STGSVSRSHDGTGVSPFAGGVEWAVTRDIAT	
Db	131 -- VYGRNHDGTGVSPFAGGVYATPEIAAT	
Qy	186 SYRFQGQDAAFPVVAAPAPAPAEVATKHTFLRK	
Db	188 SYRFQGQGAAFPVVAAPAPAPBEVQTKHTFLRK	
Qy	246 MDPKDGSAAVVLGYTDRIGSEYNQOLSEKRA	
Db	248 LDPKDGSVWVLGYTDRIGSDAYNOGISERKA	
Qy	306 GNTCDNYKQARALIDCLAPDRRVELEVKGYK	
Db	308 GNTCDNYKQARALIDCLAPDRRVELEVKGYK	
1	RESULT 4	
1	US-10-946-647-1413	
1	Sequence 1413, Application US/10946647	
1	Publication No. US/0050186217A1	
1	GENERAL INFORMATION	
1	APPLICANT: EMERY, DARYLL A.	
1	APPLICANT: STRAUB, DARREN E.	
1	APPLICANT: WONDERLING, LAURA	
1	TITLE OF INVENTION: COMPOSITIONS PRODUCED	
1	FILE REFERENCE: 253-03440101	
1	CURRENT APPLICATION NUMBER: US 10/946,647	
1	CURRENT FILING DATE: 2004-09-20	
1	PRIOR APPLICATION NUMBER: 60/504,119	
1	PRIOR FILING DATE: 2003-09-19	
1	NUMBER OF SEQ ID NOS: 1448	
1	SOFTWARE: Patentin version 3.3	
1	SEQ ID NO: 1413	
1	LENGTH: 34 6	
1	TYPE: prt	
1	ORGANISM: Escherichia coli	
1	US-10-946-647-1413	
1	Query Match	82.9% ; Score 1511;
1	Best Local Similarity	84.9% ; Pred. No. 1;
1	Matches 286; Conservative 17; Mismatch 1	
Qy	6 VLNAAPKDNTWYAGGKLGWSQYHDGFGYGNCG	
Db	18 VAGRAPKDNTWGTGAKLGWSQYHDGTFI----	

Qy 66 EMGYDWLGRMAYKGSVNDGAFKAQGVOLTAKLGYPITDDLDIYTTRLGMMWRADSKGNYA 125
 Db 73 EMGYDWLGRMAYKGSVNDGAFKAQGVOLTAKLGYPITDDLDIYTTRLGMMWRADTSN- 130
 Qy 126 STGVRSRBDTGYSPVFGVWEAVTRDIAATLEYQWNNINGDAGTIVTRPONGMISLG 185
 Db 131 ---VYGNKHDTGYSPVFGVWEAVTRDIAATLEYQWNNINGDAHTIGTRPONGMISLG 187
 Qy 186 SYRFQEDDAVPPAPAPAPEVAKHTFLKSDVLFNFKATLKPEGOALDOLYTSN 245
 Db 188 SYRFQEDDAVPPAPAPAPEVAKHTFLKSDVLFNFKATLKPEGOALDOLYTSN 247
 Qy 246 MDPKGDSAVVLGYTDRIGSEAYNQLSERKRAQSVDYLVAKGTPKAGISARGMGESENPT 305
 Db 248 LDPKGDSVVLGYTDRIGSDAYNQLSERKRAQSVDYLISKGPADKISARGMGESENPT 307
 Db 306 GNTCDNYKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342
 Db 308 GNTCDNYKQRAALIDCLAPDRRVEIEVKGYKDVVTOP 344
 Db

RESULT 5
 US-10-946-647-1448
 Sequence 1.448, Application US/10946647
 Publication No. US20050186217A1
 GENERAL INFORMATION:
 APPLICANT: STRAUB, DARREN E.
 APPLICANT: WONDERLING, LAURA
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 FILE REFERENCE: 293_00340101
 CURRENT APPLICATION NUMBER: US/10/946_647
 CURRENT FILING DATE: 2004-09-20
 PRIOR APPLICATION NUMBER: 60/504,119
 PRIOR FILING DATE: 2003-09-19
 NUMBER OF SEQ ID NOS: 1448
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 1448
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Escherichia coli

US-10-946-647-1448
 Sequence 1.448, Application US/10946647
 Publication No. US20050186217A1
 GENERAL INFORMATION:
 APPLICANT: STRAUB, DARREN E.
 APPLICANT: WONDERLING, LAURA
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 FILE REFERENCE: 293_00340101
 CURRENT APPLICATION NUMBER: US/10/946_647
 CURRENT FILING DATE: 2004-09-20
 PRIOR APPLICATION NUMBER: 60/504,119
 PRIOR FILING DATE: 2003-09-19
 NUMBER OF SEQ ID NOS: 1448
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 1448
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Escherichia coli

RESULT 5
 US-10-946-647-1448
 Sequence 1.448, Application US/10946647
 Publication No. US20050186217A1
 GENERAL INFORMATION:
 APPLICANT: STRAUB, DARREN E.
 APPLICANT: WONDERLING, LAURA
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 FILE REFERENCE: 293_00340101
 CURRENT APPLICATION NUMBER: US/10/946_647
 CURRENT FILING DATE: 2004-09-20
 PRIOR APPLICATION NUMBER: 60/504,119
 PRIOR FILING DATE: 2003-09-19
 NUMBER OF SEQ ID NOS: 1448
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 1448
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Escherichia coli

RESULT 5
 US-10-946-647-1448
 Sequence 1.448, Application US/10946647
 Publication No. US20050186217A1
 GENERAL INFORMATION:
 APPLICANT: STRAUB, DARREN E.
 APPLICANT: WONDERLING, LAURA
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 FILE REFERENCE: 293_00340101
 CURRENT APPLICATION NUMBER: US/10/946_647
 CURRENT FILING DATE: 2004-09-20
 PRIOR APPLICATION NUMBER: 60/504,119
 PRIOR FILING DATE: 2003-09-19
 NUMBER OF SEQ ID NOS: 1448
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 1448
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Escherichia coli

RESULT 6
 US-10-946-647-1377
 Sequence 1.377, Application US/10946647
 Publication No. US20050186217A1
 GENERAL INFORMATION:
 APPLICANT: STRAUB, DARREN E.
 APPLICANT: WONDERLING, LAURA
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 FILE REFERENCE: 293_00340101
 CURRENT APPLICATION NUMBER: US/10/946_647
 CURRENT FILING DATE: 2004-09-20
 PRIOR APPLICATION NUMBER: 60/504,119
 PRIOR FILING DATE: 2003-09-19
 NUMBER OF SEQ ID NOS: 1448
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 1377
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Salmonella enterica

Query Match 82.2%; Score 1499; DB 5; Length 350;
 US-10-946-647-1377
 Query Match 82.2%; Score 1499; DB 5; Length 350;

Best Local Similarity 82.8%; Pred. No 1.8e-130; Indels 6; Gaps 2; Matches 279; Conservative 26; Mismatches 26; DB 73 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 342

Qy 6 VLNAPKONTWYAGKGLGMSQYHDGTYGNGFQNNNGPTRNDGAGAFFGQVNPNLGF 65
Db 18 VAQAPKONTWYAGKLGMSQYHDGTYF1----HNDGPTHENQLAGAGAFFGQVNPNLGF 72

RESULT 9
US-10-946-647-1395
Qy 66 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 125
Db 73 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 132

Qy 126 STGVSRSSEHDGTGSPVFAGGVWAVTRDIAATRLEYQWNNNIGDAGTYGTRPDNGMLSLGV 185
Db 133 G-GASTKDIDGTGSPVFAGGIEAVTPEATRLEYQWNNNIGDANTGTRPDNGLSSVGV 191

Qy 186 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKATLKPEQGQALDOLYTOQN 245
Db 192 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKSTLKPEQGQALDOLYTOQN 251

Qy 246 MDPKDGSAVVLGYTRDGSSEANQOLSEERAQSVDYLVAKGIPAGKISARGMGESENPT 305
Db 252 LDPKDGSVVVLGFDRGDAYQGLSERASQSVVDYLISKGTPSDKISARGMGESENPT 311

Qy 306 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 342
Db 312 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 348

Qy 306 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 342
Db 312 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 348

Query Match 82.0%; Score 1495; DB 5; Length 350;
Best Local Similarity 82.8%; Pred. No 4.1e-130; Indels 6; Gaps 2; Matches 279; Conservative 26; Mismatches 26; DB 73 GNTCDNVKARAALIDCLAPDRREIEVKGYKEVVTOP 342

Qy 6 VLNAPKONTWYAGKLGMSQYHDGTYGNGFQNNNGPTRNDGAGAFFGQVNPNLGF 65
Db 18 VAQAPKONTWYAGKLGMSQYHDGTYF1----HNDGPTHENQLAGAGAFFGQVNPNLGF 72

Qy 66 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 125
Db 73 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 132

Qy 126 STGVSRSSEHDGTGSPVFAGGVWAVTRDIAATRLEYQWNNNIGDAGTYGTRPDNGMLSLGV 185
Db 133 G-GASTKDIDGTGSPVFAGGIEAVTPEATRLEYQWNNNIGDANTGTRPDNGLSSVGV 191

Qy 186 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKATLKPEQGQALDOLYTOQN 245
Db 192 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKSTLKPEQGQALDOLYTOQN 251

Qy 246 MDPKDGSAVVLGYTRDGSSEANQOLSEERAQSVDYLVAKGIPAGKISARGMGESENPT 305
Db 252 LDPKDGSVVVLGFDRGDAYQGLSERASQSVVDYLISKGTPSDKISARGMGESENPT 311

RESULT 10
US-10-946-647-1404
Qy 66 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 125
Db 73 EMGDWLGRMAYKGSVNDGAGFAKQAGVOLTAKGYPITDLDIYTRLGMMWRAKDSKNGYA 132

Qy 126 STGVSRSSEHDGTGSPVFAGGVWAVTRDIAATRLEYQWNNNIGDAGTYGTRPDNGMLSLGV 185
Db 133 G-GASTKDIDGTGSPVFAGGIEAVTPEATRLEYQWNNNIGDANTGTRPDNGLSSVGV 191

Qy 186 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKATLKPEQGQALDOLYTOQN 245
Db 192 SYRQQEADAPVWAPAPAPEVATKHTFLKSVDLFENPKSTLKPEQGQALDOLYTOQN 251

Qy 246 MDPKDGSAVVLGYTRDGSSEANQOLSEERAQSVDYLVAKGIPAGKISARGMGESENPT 305
Db 252 LDPKDGSVVVLGFDRGDAYQGLSERASQSVVDYLISKGTPSDKISARGMGESENPT 311

RESULT 12
 US-10-416-708A-27
 ; Sequence 27, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416, 708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 27
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-27

Query Match 82.0%; Score 1495; DB 5; Length 350;
 Best Local Similarity 82.8%; Pred. No. 4.1e-130;
 Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;

Qy 6 VLNAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 65
 Db 18 VAQAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 72
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 66 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADSKGNYA 125
 Db 73 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADTSKSNP 132
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 126 STCVSRSRSHDGTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNGMLSLGV 185
 Db 133 G-GPSTKDHDTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNGLSSGV 191
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 186 SYRFGQEDAAPVAPAPAPAEVATKHTLKSVDLFENFKATLKEPGQALDOLYTLQSN 245
 Db 192 SYRFGQEDAAPVAPAPAPAEVATKHTLKSVDLFENFKSTLKPQGQALDOLYLSQSN 251
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 246 MDPKDGSAAVVLGLYTDIGSEAYNQQLSEKRAQSVWDYLVAKGIPAGKLSKARGMGESENPTV 305
 Db 252 LDPKDGSAAVVLGLYTDIGSDAYNQQLSEKRAQSVWDYLISKGTPSKDSKISKARGMGESENPTV 311
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 306 GNTCDNYKARAALIDCLAPDRVEIYKGYKVVTQP 342
 Db 312 GNTCDNYKPRALAALIDCLAPDRVEIYKGYKVVTQP 348
 ; HDGPTHENOLGAGFGGYQVNPNLGF

RESULT 11
 US-10-416-708A-24
 ; Sequence 24, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416, 708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 24
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-24

Query Match 41.4%; Score 754; DB 4; Length 190;
 Best Local Similarity 79.9%; Pred. No. 1.3e-61;
 Matches 139; Conservative 9; Mismatches 9; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 65
 Db 20 VAQAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 74
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 66 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADSKGNYA 125
 Db 75 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADTSKSNP 132
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 126 STCVSRSRSHDGTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNG 179
 Db 133 --VYGRKNDHTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNG 183
 ; HDGPTHENOLGAGFGGYQVNPNLGF

RESULT 13
 US-10-416-708A-10
 ; Sequence 10, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416, 708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 10
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-10

Query Match 41.0%; Score 748; DB 4; Length 194;
 Best Local Similarity 79.8%; Pred. No. 4.9e-61;
 Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 65
 Db 20 VAQAAPKDNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDLGAGFGGYQVNPNLGF 74
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 66 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADSKGNYA 125
 Db 75 EMGYDWLGRMAYKGSVNDGAFKAQGVLTAKLGYPITDDLYTRLGGMVRADTSKSNP 132
 ; HDGPTHENOLGAGFGGYQVNPNLGF
 Qy 126 STCVSRSRSHDGTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNG 179
 Db 133 --VYGRKNDHTGVSPPVFGGVEWAATRDIATRLEYTINNNICDAGTYGTRPDNG 183
 ; HDGPTHENOLGAGFGGYQVNPNLGF

RESULT 14

US-10-416-708A-64

Sequence 64, Application US/10/16708A

Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John G.

ARTIST: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING SPECIFICITIES

FILE REFERENCE: 37779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT PUBLISHING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.2

SEQ ID NO: 64

LENGTH: 194

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthetic Construct

US-10-116-708A-64

Query Match 41.0%; Score 748; DB 4; Length 194;

Best Local Similarity 79.8%; Pred. No. 4.9%; Length 194;

Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Db 163 VRNIGDAGTVGRPDNLISLGVSYRGQEDAPVAPAPAPAPVATKHFILKSDVLFN 222

Db 60 TNNIGDAHTIGTRPDNGLISLGVSYRGQEDAPVAPAPAPVQTKHFILKSDVLFN 119

Db 223 FNKATHLKEPQGQALDQLYTQLSNMDPKDGSAVVLGTTDRIGS 264

Db 120 FNKATHLKEPQGQALDQLYTQLSNMDPKDGSVVLGTTDRIGS 161

Db 120 FNKATHLKEPQGQALDQLYTQLSNMDPKDGSVVLGTTDRIGS 161

Search completed: November 26, 2005, 00:24:11

Job time : 164 secs

RESULT 15

US-10-946-647-1436

Sequence 1436 Application US/10/946647

Publication No. US20050186217A1

GENERAL INFORMATION:

APPLICANT: EMERY, DARYL A.

APPLICANT: STRAUB, DARREN E.

APPLICANT: WONDERLING, LAURA

TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE

FILE REFERENCE: 93 0340101

CURRENT APPLICATION NUMBER: US/10/946,647

CURRENT FILING DATE: 2004-09-20

PRIOR APPLICATION NUMBER: 60/504,119

PRIOR FILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 1448

SOFTWARE: PatentIn version 3.3

SEQ ID NO: 1436

LENGTH: 161

TYPE: PRT

ORGANISM: Escherichia coli

US-10-946-647-1436

Query Match 39.5%; Score 719.5; DB 5; Length 161;

Best Local Similarity 84.6%; Pred. No. 1.7e-58;

Matches 137; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Db 103 DLDIYTRIGGMYWRADSKGNVASTGVSRSEADTGVSPFAGGVEVAVTRDIATRLEYQW 162

Protein - Protein search, using sw model

on: November 25, 2005, 23:50:22 ; Search time 188 Seconds
(without alignments)

803.970 Million cell updates/sec

title: US-09-913-772A-2

perfect score: 1823

Sequence: 1 MKAIFVINAAPKDNTWYAGG.....DRRVEIEVKGYKEVVTQPG 3 44

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 2443163 seqs, 439378781 residues

total number of hits satisfying chosen parameters: 2443163

Aar93798 Protein L 25 1026 56.3 188 2 AAR93798

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

Klebsiell Aar95645

Haemophil Aam50724

Haemophil Aam50721

Haemophil Abb83156

Partial O Sequence Aae17892

Haemophil Aam50718

Haemophil Aam50719

Haemophil Aam50717

Haemophil Aam50716

Haemophil Aam50722

Haemophil Aam50725

Haemophil Aam50720

Haemophil Aam50723

Haemophil Aam50726

Haemophil Aam50727

Virulence Aab44588

Actinobac Abp54540

Actinobac Aay97899

Actinobac Aar66294

Actinobac Aar66294

st-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries
A database : A GenBank 21.1
RESULT 1
AAB18994
ID AAB18994 standard; protein; 344 AA.
xx

SUMMARIES						
Alt No.	Score	% Query Match	Length	DB	ID	Description
1	1823	100.0	344	3	AAB18994	Aab18994 A P40 pol
2	1823	100.0	344	3	AAB08317	Aab08317 An outer
3	1823	100.0	344	3	AAY93341	Aay93341 Amino aci
4	1823	100.0	344	3	AAB08825	Aab08825 A P40 pol
5	1823	100.0	344	3	AAB18804	Aab18804 A Klebsie
6	1823	100.0	344	3	AAB08341	Aab08341 An outer
7	1823	100.0	344	4	AGK63638	Aag63638 Amino aci
8	1823	100.0	344	4	AAB67770	Aab67770 Amino aci
9	1823	100.0	344	5	AAM48395	Aam48395 Klebsiell
10	1823	100.0	344	5	AAM47796	Aam47796 Klebsiell
11	1823	100.0	344	8	AD100532	Adi100532 Klebsiell
12	1823	100.0	344	8	AD156807	Adi156807 K pneumo
13	1823	100.0	344	8	AD138366	Adi138366 K pneumo
14		99.7	344	2	AAR93797	Aar93797 Protein L
15	1818	99.7	452	4	AAB67771	Aab67771 Amino aci
16	1813	99.5	344	2	AY440771	Aay44077 K.pneumon
17	1813	99.5	344	4	AG67743	Aag67743 Amino aci
18	1813	99.5	344	4	AAB84122	Aab84122 Amino aci
19	1782	97.8	385	7	AB060934	Ab060934 Klebsiell
20	1781	97.7	335	2	AAR88257	Aar88257 K.pneumon
21	1781	97.7	335	2	AAR95644	Aar95644 Klebsiell
22	1781	97.7	335	2	AAR93796	Aar93796 Protein P
23	1289	70.7	369	6	ABM69278	Abm69278 Photorhab
24	1279	70.2	384	7	ADP07572	Adp07572 Prochlor

DR N-PSDB; AAA15498.
 XX Use of enterobacterial outer membrane protein A for delivering active
 PT substances, particularly immunogens for treating or preventing e.g.
 PT cancer, to antigen presenting cells.
 XX
 PS Claim 9; Page 28-29; 35pp; French.
 XX
 The present sequence represents a P40 protein. The protein is an outer
 CC membrane protein A (OmpA). The protein is used in pharmaceutical
 CC compositions for specific targeting of an active substance to antigen-
 CC presenting cells (APCs), especially dendritic cells. OmpA binds
 CC specifically to APCs and is internalized by them (in contrast to other
 CC protein carriers such as tetanus toxoid). The OmpA protein is used to
 CC deliver an antigen or hapten to modify (specifically to improve) an
 CC immune response, especially for treatment or prevention of cancers
 CC (particularly those that express associated antigen),
 CC autoimmune disease, allergy, graft rejection, cardiovascular or central
 CC nervous system diseases, inflammation, infection or immune deficiency
 XX
 SQ Sequence 344 AA;

Query Match, 100.0%; Score 1823; DB 3; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60
 Qy 61 PYLGFMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKLGYPTTDDLDIYTRLGGMVNRADS 120
 Db 61 PYLGFMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKLGYPTTDDLDIYTRLGGMVNRADS 120
 Qy 121 KGNYASTGVSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQVNINIDAGTVGTRPDNGM 180
 Db 121 KGNYASTGVSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQVNINIDAGTVGTRPDNGM 180
 Qy 181 LSIGVSYTRGQDAAPVYAPAPAPAPEVATKHTLKSDFVLFNFNKATLKPEGQQLDQY 240
 Db 181 LSIGVSYTRGQDAAPVYAPAPAPAPEVATKHTLKSDFVLFNFNKATLKPEGQQLDQY 240
 Qy 241 TOLSNMDPDKGSASVVLGYTRIGSEAYNQLSERKASQSVVDLVAKGIPAGKISARGME 300
 Db 241 TOLSNMDPDKGSASVVLGYTRIGSEAYNQLSERKASQSVVDLVAKGIPAGKISARGME 300
 Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344

RESULT 4
 AAB08825 standard; protein; 344 AA.
 XX
 AC AAB08825;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE A P40 polypeptide (an outer membrane protein A (OmpA)).

XX
 DE P40; outer membrane protein A; OmpA; immunogen; cytokine; growth factor;
 KW hormone; tumour-specific marker; vaccine; cancer; contraceptive.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN FR2789902-A1.
 XX
 PD 25-AUG-2000.
 XX
 PF 24-FEB-1999; 99FR-00002314.
 XX
 PR 24-FEB-1999; 99FR-00002314.

XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA XX
 PI XX
 PT Goetsch L, Corvaia N, Beck A, Haeuw JF, Bonnefoy JY;
 XX
 DR WPI; 2000-573921/54.
 DR N-PSDB; AAA75036.
 XX
 PT Use of enterobacterial outer membrane protein as immunogenic carrier,
 PT particularly for contraceptive and anti-cancer vaccines, provides strong
 PT PR particular response.
 XX
 PS Claim 5; Page 23-24; 34pp; French.
 XX
 CC The present sequence represents a P40 polypeptide of Klebsiella
 CC pneumoniae. P40 is an enterobacterial outer membrane protein A (OmpA). It
 CC can be associated an immunogen, and used to prepare a pharmaceutical
 CC composition for improving the immunological response to the immunogen.
 CC The immunogen is selected from cytokines, growth factors or hormones (or
 CC their receptors) and/or tumour-specific markers. Compositions containing
 CC OmpA induce a strong and specific antibody response. The compositions of
 CC the invention are especially useful in vaccines to prevent or treat
 CC cancer or as contraceptives.
 XX
 SQ Sequence 344 AA;
 Query Match, 100.0%; Score 1823; DB 3; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60
 Qy 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60
 Db 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60
 Qy 61 PYLGFMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKLGYPTTDDLDIYTRLGGMVNRADS 120
 Db 61 PYLGFMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKLGYPTTDDLDIYTRLGGMVNRADS 120
 Qy 121 KGNYASTGVSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQVNINIDAGTVGTRPDNGM 180
 Db 121 KGNYASTGVSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQVNINIDAGTVGTRPDNGM 180
 Qy 181 LSIGVSYTRGQDAAPVYAPAPAPAPEVATKHTLKSDFVLFNFNKATLKPEGQQLDQY 240
 Db 181 LSIGVSYTRGQDAAPVYAPAPAPAPEVATKHTLKSDFVLFNFNKATLKPEGQQLDQY 240
 Qy 241 TOLSNMDPDKGSASVVLGYTRIGSEAYNQLSERKASQSVVDLVAKGIPAGKISARGME 300
 Db 241 TOLSNMDPDKGSASVVLGYTRIGSEAYNQLSERKASQSVVDLVAKGIPAGKISARGME 300
 Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344
 Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIYKGKEVVTQPG 344

RESULT 5
 AAB18804
 ID AAB18804 standard; protein; 344 AA.
 XX
 AC AAB18804;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE A Klebsiella pneumoniae P40 polypeptide.
 KW P40 polypeptide; membrane fraction; antigen; hapten; immune response;
 KW infectious disease; cancer; paramyovirus infection;
 KW respiratory syncytial virus; parainfluenza.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN WO200054789-A1.
 PR

DE Amino acid sequence of an outer membrane protein A, P40.
 XX Outer membrane protein A; P40; antigen presenting cell; vaccine;
 KW antiviral; antibacterial; anticancer; autoimmune disease; inflammation;
 KW graft rejection; cardiovascular disease; immune deficiency.
 XX Klebsiella pneumoniae.
 OS Klebsiella pneumoniae.
 PN FR2803302-A1.
 XX DT 11-JUN-2001 (first entry)
 XX XX Amino acid sequence of an outer membrane protein A (OmpA) P40.
 DE XX ID AAB67770 standard; protein; 344 AA.
 AC AAB67770;
 XX DT 11-JUN-2001 (first entry)
 XX XX Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
 KW KW respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;
 KW vaccine.
 XX XX Klebsiella pneumoniae.
 OS OS WO200121203-A1.
 PN PN 29-MAR-2001.
 XX PD 22-SEP-2000; 2000WO-FR002626.
 XX PR 23-SEP-1999; 99FR-00011888.
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX XX Corvatae N, Goetsch L;
 PI DR WPI: 2001-257929/26.
 XX DR N-PSDB; AAH74731.
 PT XX N-PSDB; AAH74731.
 PT XX Preparing purified polypeptide soluble in absence of detergent, useful
 PT for modulating the immune system, e.g. in vaccines, by removal of
 PT detergent, denaturing and molecular sieving.
 XX PS Claim 9; Page 24-25; 34pp; French.
 XX The present sequence represents an outer membrane protein A (P40) of
 CC Klebsiella pneumoniae. The protein is soluble in aqueous solvent in
 CC absence of detergent. The specification describes a method for the
 CC preparation of this polypeptide. The P40 protein binds selectively to
 CC an antigen-presenting cell, so provides targeting, proliferation and/or
 CC expression of molecules by these cells. P40 is used, alone or as an
 CC adjuvant, to produce therapeutic compositions that are soluble in absence
 CC of detergent, especially when formulated with an antigen or hapten for
 CC modulating the host's immune system. Especially, it is used to prepare
 CC vaccines, especially antiviral, antibacterial or anticancer (e.g. against
 CC human immunodeficiency virus, respiratory syncytial virus, measles,
 CC mumps, tuberculosis etc.), but also against fungi, parasites, autoimmune
 CC diseases, graft rejection, cardiovascular disease, inflammation and
 CC immune deficiency.
 XX Sequence 344 AA;
 Score 100.0%; Score 1823; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 344 AA;
 Score 100.0%; Score 1823; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 MKAIFVLAAPKDNTWYAGKKGWQSQYHDTGFYNGNQNNNGPTRNDQLGAGAFGGYQVN 60
 Database 1 MKAIFVLAAPKDNTWYAGKKGWQSQYHDTGFYNGNQNNNGPTRNDQLGAGAFGGYQVN 60
 Query 61 PYLGFMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTTRLGGMWRA 120
 Database 61 PYLGFMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTTRLGGMWRA 120
 Query 61 KGYNASTGVSRSEHDTGVSVPFAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180
 Database 61 KGYNASTGVSRSEHDTGVSVPFAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180
 Query 181 LS LGVSYRPGQDDAAPVAPAPAPAPAVKHTFLKSDVLFNFNKTLPBQQALDQLY 240
 Database 181 LS LGVSYRPGQDDAAPVAPAPAPAVKHTFLKSDVLFNFNKTLPBQQALDQLY 240
 Query 181 TOLSNMDPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 181 TOLSNMDPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Query 241 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 241 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Query 301 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 301 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300

RESULT 8
 AAB67770
 ID AAB67770 standard; protein; 344 AA.
 XX
 AC AAB67770;
 XX DT 11-JUN-2001 (first entry)
 XX XX Amino acid sequence of an outer membrane protein A (OmpA) P40.
 DE XX Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
 KW KW respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;
 KW vaccine.
 XX XX Klebsiella pneumoniae.
 OS OS WO200121203-A1.
 PN PN 29-MAR-2001.
 XX PD 22-SEP-2000; 2000WO-FR002626.
 XX PR 23-SEP-1999; 99FR-00011888.
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX XX Corvatae N, Goetsch L;
 PI DR WPI: 2001-257929/26.
 XX DR N-PSDB; AAH80152.
 XX PR XX Vaccine against respiratory syncytial virus, comprises enterobacterial
 PT PT outer membrane protein and viral immunogen, provides protective response
 PT PR against respiratory tract. OmpA
 XX PS Claim 3; Page 28-29; 39pp; French.
 XX The present sequence represents an outer membrane protein A (OmpA),
 CC designated P40. Enterobacterium OmpA proteins, associated with an
 CC immunogenic peptide from respiratory syncytial virus (RSV), are used to
 CC prepare a nasal composition that induces a protective response, against
 CC RSV infection in the upper and lower (lung) respiratory tract. OmpA
 CC potentiates the immune response to some immunogenic peptides, eliminating
 CC the need for adjuvants. The method is useful for producing vaccines for
 CC prevention or treatment of RSV infections
 XX SQ Sequence 344 AA;
 Query Match 100.0%; Score 1823; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 MKAIFVLAAPKDNTWYAGKKGWQSQYHDTGFYNGNQNNNGPTRNDQLGAGAFGGYQVN 60
 Database 1 MKAIFVLAAPKDNTWYAGKKGWQSQYHDTGFYNGNQNNNGPTRNDQLGAGAFGGYQVN 60
 Query 61 PYLGFMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTTRLGGMWRA 120
 Database 61 PYLGFMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTTRLGGMWRA 120
 Query 61 KGYNASTGVSRSEHDTGVSVPFAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180
 Database 61 KGYNASTGVSRSEHDTGVSVPFAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180
 Query 181 LS LGVSYRPGQDDAAPVAPAPAPAVKHTFLKSDVLFNFNKTLPBQQALDQLY 240
 Database 181 LS LGVSYRPGQDDAAPVAPAPAPAVKHTFLKSDVLFNFNKTLPBQQALDQLY 240
 Query 181 TOLSNMDPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 181 TOLSNMDPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Query 241 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 241 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Query 301 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300
 Database 301 SNPVTGNTCDNPKDGSAVVLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300

Qy	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOPAG	344
Db	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOPAG	344
RESULT 9			
AAM48395	standard, protein;	344 AA.	
XX	ID	AAM47796 standard; protein; 344 AA.	
AC	AC	AAM47796;	
XX	XX	AAM47796;	
DT	DT	01-MAR-2002 (first entry)	
XX	XX	Klebsiella pneumoniae outer membrane protein, OmpA.	
DE	DE	Klebsiella pneumoniae OmpA protein.	
XX	XX	OmpA; outer membrane protein; cytosatic; cancer; tumour antigen.	
KW	KW	KW; enterobacterium; antibacterial; antifungal; antiviral; antiparasitic; antimicrobial; infection.	
XX	XX	Klebsiella pneumoniae.	
OS	OS	OS Klebsiella pneumoniae.	
XX	XX	WO200182959-A1.	
PN	PN	WO200187326-A1.	
XX	XX	22-NOV-2001.	
PD	PD	22-NOV-2001.	
XX	XX	2001WO-FR001348.	
PF	PF	16-MAY-2001; 2001WO-FR001490.	
XX	XX	PR 16-MAY-2000; 2000FR-00006199.	
PR	PR	16-MAY-2000; 2000FR-00006199.	
XX	XX	PA (FABR) FABRE MEDICAMENT SA PIERRE.	
PA	PA	XX	
XX	XX	PI Jeanmin P, Delneste Y, Baussant T;	
PI	PI	XX	
XX	XX	DR WPI; 2002-05561/07.	
XX	XX	XX Use of an enterobacterium OmpA protein for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections.	
PT	PT	XX	
PT	PT	XX	
XX	XX	XX	
PS	PS	Claim 8; Page 24-25; 33pp; French.	
XX	XX	The present sequence is OmpA protein from enterobacteria Klebsiella pneumoniae. OmpA protein can be used to prepare an antimicrobial pharmaceutical composition for mucosal delivery. The composition can be used for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections	
XX	XX	XX	
SQ	SQ	Sequence 344 AA;	
RESULT 10			
AAM47796	standard, protein;	344 AA.	
XX	XX	AAM47796;	
AC	AC	AAM47796;	
XX	XX	03-MAY-2001; 2001WO-FR001348.	
PR	PR	04-MAY-2000; 2000FR-00005702.	
XX	XX	XX	
PA	PA	(FABR) FABRE MEDICAMENT SA PIERRE.	
XX	XX	XX	
PI	PI	XX	
XX	XX	DR WPI; 2002-056490/09.	
XX	XX	XX Composition, useful for treatment and prevention of cancer, also for detecting tumor antigens, comprises an outer membrane protein and tumor lysate.	
PT	PT	XX	
PT	PT	XX	
XX	XX	XX	
PS	PS	Claim 5; Page 25-26; 32pp; French.	
XX	XX	The present invention relates to a pharmaceutical composition, comprising an Outer Membrane Protein (e.g. OmpA), associated with a lysate of autologous and/or heterologous tumour cells. The present sequence is one such OmpA from Klebsiella pneumoniae. The composition is useful for the treatment of cancers, particularly where associated with tumour antigens, and for detecting tumour antigens	
XX	XX	XX	
SQ	SQ	Sequence 344 AA;	
RESULT 11			
Qy	1	1 MKAIFVINAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTTRDOLGAGAFGGYQVN	60
Db	1	1 MKAIFVINAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTTRDOLGAGAFGGYQVN	60
Qy	1	61 PYLGFMGYDMLGRMAYKGSVNDGAFAQGVQVLAQKUGYPTTDDLYTRUGGMVRADS	120
Db	61	61 PYLGFMGYDMLGRMAYKGSVNDGAFAQGVQVLAQKUGYPTTDDLYTRUGGMVRADS	120
Qy	61	61 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Db	61	61 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Qy	121	121 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Db	121	121 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Qy	121	121 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Db	121	121 KGNYASTGVRSSEHDTGSPVFAGGVWAVTRDIATRLEYQWNNIGDAGTVTRPDNGM	180
Qy	181	181 LSLGVSYRFQDAAVLPVAPAPAPAEVATKHTLKSVDLFENFKATLKPGCQQADQLY	240
Db	181	181 LSLGVSYRFQDAAVLPVAPAPAPAEVATKHTLKSVDLFENFKATLKPGCQQADQLY	240
Qy	181	181 LSLGVSYRFQDAAVLPVAPAPAPAEVATKHTLKSVDLFENFKATLKPGCQQADQLY	240
Db	181	181 LSLGVSYRFQDAAVLPVAPAPAPAEVATKHTLKSVDLFENFKATLKPGCQQADQLY	240
Qy	241	241 TQLSNMDPKDGSAVVLPGYTRIGSEAYNQLESEKRAVSVDYLVAKGIPAGKISARGMGE	300
Db	241	241 TQLSNMDPKDGSAVVLPGYTRIGSEAYNQLESEKRAVSVDYLVAKGIPAGKISARGMGE	300
Qy	241	241 TQLSNMDPKDGSAVVLPGYTRIGSEAYNQLESEKRAVSVDYLVAKGIPAGKISARGMGE	300
Db	241	241 TQLSNMDPKDGSAVVLPGYTRIGSEAYNQLESEKRAVSVDYLVAKGIPAGKISARGMGE	300
Qy	301	301 SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOPAG	344
Db	301	301 SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOPAG	344

Qy	241 TQLSNMDPKDGSAAVILGYTDRIGSEAYNQOLSEKRAQSVDYLVAKGIPAKISARGMGE 300
Db	241 TQLSNMDPKDGSAAVILGYTDRIGSEAYNQOLSEKRAQSVDYLVAKGIPAKISARGMGE 300
Qy	301 SNPVTGNTCDNVKARAA1IDCLAPDRRVEIUVKGYKEVUTQPG 344
Db	301 SNPVTGNTCDNVKARAA1IDCLAPDRRVEIUVKGYKEVUTQPG 344
RESULT 11	
ID AD100532	standard; protein: 344 AA.
XX	
AC AD100532;	
XX	
DT 15-APR-2004	(first entry)
XX	
DE Klebsiella pneumoniae OmpA P40 protein.	
XX	
KW solubility; virucide; antibacterial; parasiticide; fungicide; cytostatic;	
KW vaccine; viral; bacterial; parasitic; fungal infection; cancer;	
KW gene therapy; cosmetic; major histocompatibility complex; MHC;	
KW cytotoxic T lymphocyte; CTL; OmpA; P40.	
OS Klebsiella pneumoniae.	
XX	
PN FR2842812-A1.	
XX	
PD 30-JAN-2004.	
XX	
PF 26-JUL-2002; 2002FR-00009526.	
XX	
PR 26-JUL-2002; 2002FR-00009526.	
XX	
(FABR) FABRE MEDICAMENT SA PIERRE.	
XX	
PA Beck A, Corvai N, Klinguer HC, Goetsch L;	
XX	
DR 2004-135597/14.	
XX	
PS Disclosure; SEQ ID NO 72; 65pp; French.	
XX	
PS Solubilizing hydrophobic peptides, useful e.g. in vaccines against	
PT infectious microbes or tumors, by attachment of at least three lysine	
PT residues.	
XX	
CC The invention relates to a novel method for solubilising, or improving	
CC the solubility of, a peptide in aqueous medium comprising covalent	
CC attachment of at least 3 residues of Lys, in L or D form, distributed	
CC over the N and/or C termini in the form of a linear or branched chain.	
CC The invention has virucide, antibacterial, parasiticide, fungicide and	
CC cytostatic activities and may be used to generate prophylactic or	
CC therapeutic vaccines or compositions for control of viral, bacterial,	
CC parasitic or fungal infections or cancers, as well as during gene therapy	
CC procedures. The peptides of the invention may also be used in cosmetic	
CC compositions. The current sequence is that of the Klebsiella pneumoniae	
CC OmpA P40 protein of the invention.	
XX	
SQ Sequence 344 AA;	
Query Match Score 1823; DB 8; Length 344;	
Best Local Similarity 100.0%; Pred. No. 1.3e-157;	
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 MKAIFVLNAAPKDNTWYAGGKLGWSOYHTDGFYNGFQNNNGPTNDOLGAGAFTGGYQVN 60	
Db 1 MKAIFVLNAAPKDNTWYAGGKLGWSOYHTDGFYNGFQNNNGPTNDOLGAGAFTGGYQVN 60	
Qy 61 PYLGFENGYDNLGRMAYGSVNGFAKAQGQVLTAKUGYPITDDLYTRLGGMWRADS 120	
Db 61 PYLGFENGYDNLGRMAYGSVNGFAKAQGQVLTAKUGYPITDDLYTRLGGMWRADS 120	
Qy 121 KGNYASTGVSRSEHDTSVSPVAGGGEWAATVRDIATRLQYQNNNGDAGTYGTRPDNGM 180	
Db 121 KGNYASTGVSRSEHDTSVSPVAGGGEWAATVRDIATRLQYQNNNGDAGTYGTRPDNGM 180	
Qy 181 LSLGVSYRFGQDAAPYVAPAPAPAPVATKHTLKSVDLFNPKATLKPEQGQALDOLY 240	
Db 181 LSLGVSYRFGQDAAPYVAPAPAPAPVATKHTLKSVDLFNPKATLKPEQGQALDOLY 240	
Qy 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db Sequence 344 AA;	
Query Match Score 1823; DB 8; Length 344;	
Best Local Similarity 100.0%; Pred. No. 1.3e-157;	
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Query	Match	Score	DB	Length
1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	100 0%	Score 1823 ; Pred. No. 1.3e-157;	Length 344 ;
1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	100 0%	Score 1823 ; Pred. No. 1.3e-157;	Length 344 ;
1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	1 MKAJFVINAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	100 0%	Score 1823 ; Pred. No. 1.3e-157;	Length 344 ;
61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	Qy 1 MKAIFVNAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	1 MKAIFVNAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	
61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	Db 1 MKAIFVNAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	1 MKAIFVNAAPKDNTWYAGKLGWSQYHDTGFCNGFQNNINGPRNDLQAGAAGFQYQVN 60	
121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	Qy 61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	
121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	Db 61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	61 PYLGFMGYDWLGRMAYKGSVDNGAFAQVQTLAKGYPTTDDLDIYTRLGVMWRADS 120	
181 LSUGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	181 LSUGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	Qy 121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	
181 LSUGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	181 LSUGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	Db 121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	121 KGNYASTGVSRSEHDGTGSPVFAGGWEAVTRDIAFTRLEYQWNNNGDAGTGVTRPDGM 180	
241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	Qy 181 LSLGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	181 LSLGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	
241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	Db 181 LSLGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	181 LSLGVSYRFQGEDAAPVWAPAPAPAPAVATKHFTRLSDVLFENFKATLKPEGQALDQY 240	
301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	Qy 241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	
301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	Db 241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	241 TQLSNMDPKDGSAVVILGYTRIGSEBAYNQOLSEKRAQSVDYLVAKGIPAGKTSARGMGB 300	
RESULT 13		Qy 301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	
ID AD138366	standard; protein; 344 AA.	Db 301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	301 SNPVTGNTCDNVKARALIDCLAPDRRYVEIIVGKYEKVVTQPG 344	
RESULT 14		RESULT 14		
AC AD138366;		AAR93797		
AC XX	22-APR-2004 (first entry)	ID AAR93797 standard; protein; 344 AA.		
AC XX		XX AAR93797;		
DS XX		AC AAR93797;		
XX K. pneumoniae OmpA P40, seq id 2.		XX		
XX Cytostatic; vaccine; beta-hCG; human chorionic gonadotropin; beta-chain; cytotoxic T lymphocyte; CTL; cancer; OmpA; P40.		DT 16-SEP-1998 (first entry)		
XX Homo sapiens.		XX Protein LP40, a variant of OmpA protein P40 from K. pneumoniae I-145.		
OS XX		DE KW Outer membrane protein; OmpA; P40; immunocomplex; oligosaccharide; polysaccharide; vaccine; Salmonella.		
OS PN		XX Synthetic.		
PN XX		OS Klebsiella pneumoniae.		
PN XX		XX		
PD 14-NOV-2003.		PD 13-NOV-1997.		
PD 07-MAY-2002; 2002FR-00005691.		XX		
PF 07-MAY-2002; 2002FR-00005691.		PF 06-MAY-1997; 97WO-FR000800.		
PR 07-MAY-2002; 2002FR-00005691.		XX		
PR 07-MAY-1996; 96FR-00005692.		PR 07-MAY-1996; 96FR-00005692.		
XX		XX		
PA (FABR) FABRE MEDICAMENT SA PIERRE.		PA (FABR) FABRE MEDICAMENT SA PIERRE.		
PA XX		XX		
PT XX		PT 06-MAY-1997; 97WO-FR000800.		
PT XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PS PA (FABR) FABRE MEDICAMENT SA PIERRE.		
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PS XX		PT 06-MAY-1997; 97WO-FR000800.		
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PS XX		PT 06-MAY-1997; 97WO-FR000800.		
PS XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PT 06-MAY-1997; 97WO-FR000800.		
PS XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PT 06-MAY-1997; 97WO-FR000800.		
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PS XX		PT 07-MAY-1996; 96FR-00005692.		
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PS XX		PA PA (FABR) FABRE MEDICAMENT SA PIERRE.		
PS XX		XX		
PS XX		PT 06-MAY-1997; 97WO-FR000800.		
PS XX		PT 07-MAY-1996; 96FR-00005692.		

CC *S. enteritidis*, *S. panama* and *S. dublin*. A vaccine prepared using an CC oligosaccharide from *S. enteritidis* can be used to provide protection against septicæmia caused by *S. typhi* and against typhoid fever, as well CC as to protect humans and animals from toxic infections and zoonosis caused by *Salmonella* of the same serogroup. The carrier proteins enhance CC the immunogenicity of the oligo- or polysaccharide antigens, such as the *Vi* antigen, increases CC additional *Salmonella* capsule antigens, such as the *Vi* antigen, increases CC the vaccine's efficacy against encapsulated bacteria. The present CC sequence, protein LP40, is a preferred example of a carrier protein which CC can be used in the immunocomplex. It is obtained by recombinant CC expression of a modified *Kleb. pneumoniae* I-145 P40 gene in *E. coli*

XX Sequence 344 AA;

Query Match 99.7%; Score 1818; DB 2; Length 344;

Best Local Similarity 99.7%; Pred. No. 3 6e-157; 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKAIFVINAAPKDNTWAGKLGWSQYHDTGPGYNGFQNNGPTRNDLGAAGFGGYQVN 60

Db 1 MKAIFVINAAPKDNTWAGKLGWSQYHDTGPGYNGFQNNGPTRNDLGAAGFGGYQVN 60

Qy 61 PYLGPFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKGYPIIDLDLYTRLGGMWRAIDS 120

Db 61 PYLGPFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKGYPIIDLDLYTRLGGMWRAIDS 120

Qy 121 KGNYASTGVSRSEHDGTGVSPIVAGGVENAVTRDIATRLEYQWNNNGDAGTYGTRPDNGM 180

Db 121 KGNYASTGVSRSEHDGTGVSPIVAGGVENAVTRDIATRLEYQWNNNGDAGTYGTRPDNGM 180

Qy 181 LSLGVSYRFGQDAPIVYAPAPAPEVATKHTFLKSDVLENFKATLKEPGQALDOLY 240

Db 181 LSLGVSYRFGQDAPIVYAPAPAPEVATKHTFLKSDVLENFKATLKEPGQALDOLY 240

Qy 241 TOLSNMDPKDGSAVVILGYTDRIGSEANQNQLESEKRAQSVDYLVAKGIPAKGKSARGME 300

Db 241 TOLSNMDPKDGSAVVILGYTDRIGSEANQNQLESEKRAQSVDYLVAKGIPAKGKSARGME 300

Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTOPAG 344

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTQPQG 344

RESULT 15

XX AAB67771 standard, protein; 452 AA.

AC AAB67771;

XX DT 11-JUN-2001 (first entry)

DE Amino acid sequence of a fusion protein of P40 and RSV antigen.

XX KW Outer membrane protein A; OMPA; P40; enterobacteria; nasal composition;

XX RSV; RSV infection; lung; respiratory tract; vaccine.

OS Synthetic.

OS *Klebsiella pneumoniae*.
OS Respiratory syncytial virus.

XX PN W0200121203-A1.

PD 29-MAR-2001.

XX PF 22-SEP-2000; 2000WO-FR002626.

XX PR 23-SEP-1999; 99FR-00011888.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX Corvaiea N, Goesch L;

XX WPI; 2001-257929/26.

DR N-PSDB; AAF80153.

XX Vaccine against respiratory syncytial virus, comprises enterobacterial PT outer membrane protein and viral immunogen, provides protective response PT throughout the respiratory tract.

XX Example 2; Page 31-32; 39pp; French.

CC The present sequence represents a fusion protein comprising a *Klebsiella* CC pneumoniae outer membrane protein A (OMP) designated P40 and a CC respiratory syncytial virus (RSV) antigen. Enterobacterium OMPA proteins, CC associated with an immunogenic peptide from RSV are used to prepare a CC nasal composition that induces a protective response against RSV CC infection in the upper and lower (lung) respiratory tract. OMPA CC potentiates the immune response to some immunogenic peptides, eliminating CC the need for adjuvants. The method is useful for producing vaccines for CC prevention or treatment of RSV infections

XX SQ Sequence 452 AA;

Query Match 99.7%; Score 1818; DB 4; Length 452;
Best Local Similarity 99.7%; Pred. No. 5 4e-157;
Matches 343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKAIFVINAAPKDNTWAGKLGWSQYHDTGPGYNGFQNNGPTRNDLGAAGFGGYQVN 60

Db 1 MKAIFVINAAPKDNTWAGKLGWSQYHDTGPGYNGFQNNGPTRNDLGAAGFGGYQVN 60

Qy 61 PYLGPFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKGYPIIDLDLYTRLGGMWRAIDS 120

Db 61 PYLGPFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKGYPIIDLDLYTRLGGMWRAIDS 120

Qy 121 KGNYASTGVSRSEHDGTGVSPIVAGGVENAVTRDIATRLEYQWNNNGDAGTYGTRPDNGM 180

Db 121 KGNYASTGVSRSEHDGTGVSPIVAGGVENAVTRDIATRLEYQWNNNGDAGTYGTRPDNGM 180

Qy 181 LSLGVSYRFGQDAPIVYAPAPAPEVATKHTFLKSDVLENFKATLKEPGQALDOLY 240

Db 181 LSLGVSYRFGQDAPIVYAPAPAPEVATKHTFLKSDVLENFKATLKEPGQALDOLY 240

Qy 241 TOLSNMDPKDGSAVVILGYTDRIGSEANQNQLESEKRAQSVDYLVAKGIPAKGKSARGME 300

Db 241 TOLSNMDPKDGSAVVILGYTDRIGSEANQNQLESEKRAQSVDYLVAKGIPAKGKSARGME 300

Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTOPAG 344

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTQPQG 344

Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTQFQG 344

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYKGYKEVVTQFQG 344

Search completed: November 26, 2005, 00:05:49
Job time : 192 secs

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OM protein - protein search, using sw mode1

Run on: November 26, 2005, 00:03:28 ; Search time 46 Seconds
(without alignments)

618-270 Million cell updates/sec

Title: US-09-913-772a-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAAPKDNNTWYAGG.....DRVIEVKYKEVVTQPG 344

Scoring table: BLOSUM62

Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:
* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1782	97.8	385	2 US-09-489-039A-7451	Sequence 7451, Ap
2	1781	97.7	335	2 US-08-836-500A-2	Sequence 2, Ap
3	1781	97.7	335	2 US-09-679-750-2	Sequence 2, Ap
4	1219	70.2	384	2 US-09-543-681A-7922	Sequence 7922, Ap
5	984	54.0	179	2 US-08-836-500A-4	Sequence 4, Ap
6	984	54.0	179	2 US-09-679-750-4	Sequence 4, Ap
7	671	36.8	364	2 US-09-809-665A-151	Sequence 151, Ap
8	667	36.6	364	2 US-09-418-980-8	Sequence 8, Ap
9	667	36.6	364	2 US-09-506-078-45	Sequence 45, Ap
10	662	36.3	359	1 US-08-457-997B-2	Sequence 2, Ap
11	662.5	36.3	359	2 US-08-467-722A-2	Sequence 2, Ap
12	662.5	36.3	359	2 US-09-451-184-2	Sequence 2, Ap
13	646.5	35.5	369	2 US-09-809-665A-153	Sequence 153, Ap
14	639.5	35.1	369	2 US-09-418-980-10	Sequence 10, Ap
15	639.5	35.1	369	2 US-09-506-078-46	Sequence 46, Ap
16	586.5	32.2	338	1 US-08-210-394-1	Sequence 1, Ap
17	379	20.8	72	2 US-08-836-500A-6	Sequence 6, Ap
18	379	20.8	72	2 US-09-679-750-6	Sequence 6, Ap
19	281	15.4	53	2 US-08-836-500A-8	Sequence 8, Ap
20	281	15.4	53	2 US-09-679-750-8	Sequence 8, Ap
21	242.5	13.3	379	2 US-09-328-352-5219	Sequence 5219, Ap
22	231.5	12.7	351	2 US-09-523-991A-0094	Sequence 2, Ap
23	224.5	12.3	349	2 US-09-573-630A-2	Sequence 2, Ap
24	200	11.0	342	2 US-09-905-540-15847	Sequence 15847, Ap
25	193.5	10.9	235	2 US-09-328-352-5775	Sequence 5775, Ap
26	193.5	10.6	259	2 US-09-328-352-6621	Sequence 6621, Ap
27	184.5	10.1	566	2 US-09-489-039A-14179	Sequence 14179, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-7451
; Sequence 7451, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 270/9 2004001
; CURRENT APPLICATION NUMBER: US/09/489-039A
; CURRENT FILING DATE: 2000-01-27
; PRIORITY APPLICATION NUMBER: US 60/117,747
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 7451
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-7451

Query Match 97.8%; Score 1782; DB 2; Length 385;
Best Local Similarity 99.4%; Pred. No. 4.3e-169;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 VLNAAPKDNNTWYAGGKLGWSQYHDGTYGNGFQNNNGPTRNDLGAGFGGYQVNPTYLG 65
Qy Db 47 VAOAPKDNNTWYAGGKLGWSQYHDGTYGNGFQNNNGPTRNDLGAGFGGYQVNPTYLG 106
66 ENGYDNGRMAYKGSVNDNGAFAQGIVQTLAKGYPYDLDIYTRLGGMVWADSKGNYA 125
Qy Db 107 ENGYDNGRMAYKGSVNDNGAFAQGIVQTLAKGYPYDLDIYTRLGGMVWADSKGNYA 166
126 STGVSRSEHDGTGSPVPGAGVMAVTDIATLEYQVNNTGDAFTGTRPDNGMISLGV 185
Qy Db 167 STGVSRSEHDGTGSPVPGAGVMAVTDIATLEYQVNNTGDAFTGTRPDNGMISLGV 226
186 SYRGQDAAPVAPAPAPAPAVATKPFQSCQALDQLYTOLSN 245
Qy Db 227 SYRGQDAAPVAPAPAPAPAVATKPFQSCQALDQLYTOLSN 286
246 MDPKDGSAVVLYGTDIGSEAYNQQLSEKRAQSYYLVAKGIPACKSISARGMGEVNPTV 305
Qy Db 287 MDPKDGSAVVLYGTDIGSEAYNQQLSEKRAQSYYLVAKGIPACKSISARGMGEVNPTV 346
306 GNTCDNTVKARALIDCLAPDRVEIETGYKEVNTQPA 343
Qy Db 347 GNTCDNTVKARALIDCLAPDRVEIETGYKEVNTQPA 384
RESULT 2

```

US-08-836-500A-2
; Sequence 2, Application US/08836500A
; Patent No. 6,197929
; GENERAL INFORMATION:
; APPLICANT: Bausant, Thierry
; APPLICANT: Haew, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6,197929

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; STREET: 4700
; CITY: Chicago
; STATE: Illinois
; ZIP: 60601
; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: P1E1514P0180US
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: P1E1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-500A-2

Query Match          97.7%; Score 1781; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4-4e-169;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy          10 APKDNNTWYAGGKGKLNQSOYHDTGFGYGNQFQNNNGPTRNDQLAGAGFGQYQVNPNYLGFEMGY 69
Qy          1 APKDNNTWYAGGKGKLNQSOYHDTGFGYGNQFQNNNGPTRNDQLAGAGFGQYQVNPNYLGFEMGY 60
Db          70 DWLGRNAYKGSVDNGFKAKAQVQLPAKLGPITDLDIYTRLGGMWWRADSKGNYASTGV 129
Db          61 DWLGRNAYKGSVDNGFKAKAQVQLPAKLGPITDLDIYTRLGGMWWRADSKGNYASTGV 120
Qy          130 SRSEHDTGVSFVFGGVEAWTRDIASTRLEYQWNNGIDAGTVGTRPDNGMLSLGVSYRF 189
Db          121 SRSEHDTGVSFVFGGVEAWTRDIASTRLEYQWNNGIDAGTVGTRPDNGMLSLGVSYRF 180
Qy          190 QGEDAAPPVAPAPAPAPEVATKHTFLKSDVLFNPKATLKPEGQDQLDOLYTLQSLNMDPK 249
Db          181 QGEDAAPPVAPAPAPAPEVATKHTFLKSDVLFNPKATLKPEGQDQLDOLYTLQSLNMDPK 240
Qy          250 DGSAVLVGYTRIGSAYNQSLSEKRAQSVDYLVKGIPAKG1SARGCESNPVNTGNTC 309
Db          241 DGSAVLVGYTRIGSAYNQSLSEKRAQSVDYLVKGIPAKG1SARGCESNPVNTGNTC 300
Qy          310 DNVKARAA1IDCLAPRVELEVKG1KEVITQPG 344
Db          301 DNVKARAA1IDCLAPRVELEVKG1KEVITQPG 335

```

RESULT 3
 US-09-679-750-2
 ; Sequence 2, Application US/09679750
 ; Patent No. 6780420
 ; GENERAL INFORMATION:
 APPLICANT: BINZ, Hans
 Bausant, Thierry
 Haeuw, Jean-Francois
 Nguyen Ngoc, Thien
 TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines
 ; Patent No. 6780420
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
 STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/679,750
 FILING DATE: 08-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/836,500
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kat, Martin L.
 REGISTRATION NUMBER: 25,011
 REFERENCE/DOCKET NUMBER: PIB1514P0180US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 335 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-679-750-2
 Query Match 97.7%; Score 1781; DB 2; Length 335;
 Best Local Similarity 100.0%; Pred. No. 4.4e-169;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 APKDNTWYAGKGLGWQSQYHDTGFYNGFQNNGPTRNDLQAGAAGFGGYQNPNLGFEMGY 69
 Db 1 APKDNTWAGKGLGWQSQYHDTGFYNGFQNNGPTRNDLQAGAAGFGGYQNPNLGFEMGY 60
 Qy 70 DNIGRMAYKGVDNGAFAQGVQLTAKGYPTPDDLDYTQLGEMWRAQSKGNVASTGV 129
 Db 61 DNIGRMAYKGVDNGAFAQGVQLTAKGYPTPDDLDYTQLGEMWRAQSKGNVASTGV 120
 Qy 130 SKSEHDIGVSPYFAGGVWAVTRDIATLEYQWNNIGDAGTGYTRPDNGMLSLGVSYRF 189
 Db 121 SKSEHDIGVSPYFAGGVWAVTRDIATLEYQWNNIGDAGTGYTRPDNGMLSLGVSYRF 180
 Qy 190 GOEDAIPVVAAPAPAPPEVAKHTFLKSQVLFNFKATLKEPEGQOALDQYTLQNSMDPK 249
 Db 181 QGDEAIPVVAAPAPAPPEVAKHTFLKSQVLFNFKATLKEPEGQOALDQYTLQNSMDPK 240
 Qy 250 DGSAYVILGTYDRIGTSEAYNOQLSEKRAQSVDYLVAKGIPAKTSARGCESNPVGTNTC 309

RESULT 4

US-09-543-681A-7922

Sequence 7922, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7922

LENGTH: 384

TYPE: PRT

ORGANISM: *Proteus mirabilis*

US-09-543-681A-7922

Query Match 70.2%; Score 1279; DB 2; Length 384;

Best Local Similarity 70.5%; Pred. No. 6.4e-119;

Matches 243; Conservative 32; Mismatches 59; Indels 6; Gaps 3;

Query 9 AAPKDNTWYAGGKGKLGWSQYHDTGFGYGNFGQNNGPTRNDQLGAGAFCGGYQVNPNYLGFEMG 68

Db 43 AAPKDNTWYAGGKGKLGWSQYHDTGFGYGNFGQNNGPTRNDQLGAGAFCGGYQVNPNYLGFELG 102

Db 43 AAPKDNTWYAGGKGKLGWSQYHDTGFGYGNFGQNNGPTRNDQLGAGAFCGGYQVNPNYLGFELG 69

Qy 69 YDWLGRMAWKGSVNGAFAKQGVLVTAKGYPITDDLDITYTRUGGMWRADESKG--NVA 126

Db 103 YDWLGRMAWKGSVNGAFAKQGVLVTAKGYPITDDLDITYTRUGGMWRADESTATINAT 162

Db 127 TGVSRL--SHDGTGVSVPFGVGGVVAITRDIATRLYQWNNICDAGTYTRPQNGMISLG 184

Db 163 AGTKRFSNDTGVSVPFGVGGVVAITRDIATRLYQWNNICDAGTYTRPQNGMISLG 222

Qy 185 VSVYRGQEDAAVYVAPAP--APABEVATHFTLKDSDLFNFENKATLKPEGQQLDOLYQ 242

Db 223 VAYRFNQETPAPVTEPAPVAPAEVNTKFTLRSVLFNYYNSKLXAEQEALNGLYNE 282

Qy 243 LSNNIDPKDQDSAVAVLGYTDIGSEAYNQOQSERKAQSVVYDLYVARGIPAKGKISARGMGEN 302

Db 283 LANIDPTQGRVVVIGYTRDQGSONYNLPSERQASVYDLYVSKGIPANISIAERGKEN 342

Qy 303 PVTGNTCDNPKARALIDCLAPDRVEIYKGYKSEVYTOP 342

Db 343 PVTGNTCDNPKARALIDCLAPDRVEIYGTTEVYVQOP 382

RESULT 5

US-08-836-500A-4

Sequence 4, Application US/08836500A

Patent No. 6197929

GENERAL INFORMATION:

APPLICANT: Binz, Hans

APPLICANT: Baussant, Thierry

APPLICANT: Haeuw, Jean-Francois

APPLICANT: Nguyen Ngoc, Thien

TITLE OF INVENTION: Carrier Protein Having an Adjuvant

TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for

TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines

TITLE OF INVENTION: Carrier Protein Having an Adjuvant

TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for

TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines

Patent No. 6780420

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

APPLICANT: Binz, Hans

APPLICANT: Baussant, Thierry

APPLICANT: Haeuw, Jean-Francois

APPLICANT: Nguyen Ngoc, Thien

APPLICANT: Rockey, Milnamow & Katz, Ltd.

ADDRESS: 180 N. Stetson, 2 Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/679,750
 FILING DATE: 08-OCT-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/836,500
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Katz, Martin L.
 REGISTRATION NUMBER: 25,011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5600
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-679-750-4

Query Match 54.0%; Score 984; DB 2; Length 179;
 Best Local Similarity 100.0%; Pred. No. 5.4e-90; Length 179;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKONTWAGKLGWSQHDTGFGNGFQNNNGPTRNDQAGAAGGGVQNPYLGFMGY 69
 Db 1 APKONTWAGKLGWSQHDTGFGNGFQNNNGPTRNDQAGAAGGGVQNPYLGFMGY 60

Qy 70 DWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTIDLDIYTRLGMMWNRADSKCNYASTGV 129
 Db 61 DWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTIDLDIYTRLGMMWNRADSKCNYASTGV 120

Qy 130 SRSEHDGTGSPVFGGVEWAVTRDIATLEYQWNNNGDAGTGYTRPDNGMISLGVSYR 188
 Db 121 SRSEHDGTGSPVFGGVEWAVTRDIATLEYQWNNNGDAGTGYTRPDNGMISLGVSYR 179

RESULT 7
 US 09-809-665A-151
 Sequence 151, Application US/09809665A
 PRIORITY INFORMATION:
 APPLICANT: Lowry E., David, et al.
 FILE REFERENCE: 28341/00435
 CURRENT APPLICATION NUMBER: US/09/809,665A
 CURRENT FILING DATE: 2001-03-15
 PRIOR APPLICATION NUMBER: 60/153,453
 PRIOR FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: 60/128,689
 PRIOR FILING DATE: 1999-04-09
 PRIOR APPLICATION NUMBER: 09/545,199
 PRIOR FILING DATE: 2000-04-06
 NUMBER OF SEQ ID NOS: 197
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 151
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Actinobacillus pleuropneumoniae
 US-09-809-665A-151

Query Match 36.8%; Score 671; DB 2; Length 364;
 Best Local Similarity 42.4%; Pred. No. 2.6e-58; Length 364;
 Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNNTWAGKLGWSQHDTGFGNGFQNNNGPTR---NDOLGAGAGFG 56
 Db 11 LSAAVAQAPQQTYYAGAKGWA\$HIGE\$QD\$AKNTDRTGKYGINRNSVTYGVFGG 70

Qy 57 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVQVLTAKLGYPTIDLD 106
 Db 71 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVQVLTAKLGYPTIDLD 106

Query Match 36.6%; Score 667; DB 2; Length 364;
 Best Local Similarity 42.1%; Pred. No. 6.5e-58; Length 364;
 Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;
 SEQ ID NO: 8

Query Match 36.6%; Score 667; DB 2; Length 364;
 Best Local Similarity 42.1%; Pred. No. 6.5e-58; Length 364;
 Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNNTWAGKLGWSQHDTGFGNGFQNNNGPTR---NDOLGAGAGFG 56
 Db 11 LSAAVAQAPQQTYYAGAKGWA\$HIGE\$QD\$AKNTDRTGKYGINRNSVTYGVFGG 70

Qy 107 YTRLG-GMWRADSKCNYASTGVSRSEHDGTGSPVFGGVEWAVTRDIATLEYQWNN 165
 Db 131 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVQVLTAKLGYPTIDLD 106

Query Match 36.8%; Score 671; DB 2; Length 364;
 Best Local Similarity 42.4%; Pred. No. 2.6e-58; Length 364;
 Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNNTWAGKLGWSQHDTGFGNGFQNNNGPTR---NDOLGAGAGFG 56
 Db 11 LSAAVAQAPQQTYYAGAKGWA\$HIGE\$QD\$AKNTDRTGKYGINRNSVTYGVFGG 70

Qy 57 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVQVLTAKLGYPTIDLD 106

Db 302 TVANYIVSKGAPAAVNTAVGYGEANPVTGATCDKVKGKALIACLAPDRRVEQVQGTKE 361
 Qy 338 V 338
 Db 362 V 362

RESULT 9
 Sequence 45, Application US/09506078
 Patent No. 6911206
 CURRENT APPLICATION NUMBER: US/09/506,078
 CURRENT FILING DATE: 2000-02-16
 EARLIER APPLICATION NUMBER: N/A
 EARLIER FILING DATE: 1999-02-17
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 45
 LENGTH: 364
 TYPE: PRT
 ORGANISM: *Actinobacillus pleuropneumoniae*
 US-09-506-078-45

Query Match 36.6%; Score 667; DB 2; Length 364;
 Best Local Similarity 42.1%; Pred. No. 6 5e-58;
 Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVLAAPKDNITYAGKLGKQYNTGFGVNGPQNNGPTR----NDQLGAGAFGG 56
 Db 11 LSAAVAQAPQNTFYAGAKAGWASFHGGIEQQLDSAKNTDQTKYGINRNSVTYGFEG 70
 Qy 57 YQV--NPVLF--EMGYDWLGRM--AYKGSDVNGAPK--AQGVQTLAKLGYPITDDLD 106
 Db 71 YQINQDKLGLAAELGYDYFGRVRSKSEKNGRADKKTFRHAAGTIALKPSYEVLPD 130
 Qy 107 IYRLRG-GWWRADSKGNASTGVSRSEIDTGVPVAGGVENAVTRDIATRLEYQVN 165
 Db 131 VYGRVGTIALVNTYKTENDAQEVKTRRQS--SLILGAGVETAILPPLAARVEYQVN 188
 Qy 166 IGDA-----GTVGTRDNGMILSGLGSYRFQEDAAPPVAPAPAPEVATKHTFLKS 217
 Db 189 AGKASYSTUNRMGATDYSIISVAGLQYRFEG-GATVAAPA----VETKNAFAS 241
 Qy 218 DVLPNENKATLKPQGQDQLQYMTOLSNDPKDGSAVVLYGTDIGSEANQOLSEKRAQ 277
 Db 242 DVLPAFGSKSNLKPAAATALDAMQTEINRNLGSNAIQYQNGYDRIGEAKSNLKSQRAE 301
 Qy 278 SVVDYLVAKGIPACKISARGMGESNPVGTGTCDNVKARAALIDCLAPDRRVELEVGYK 337
 Db 302 TVANYIVSKGAPAAVNTAVGYGEANPVTGATCDKVKGKALIACLAPDRRVEQVQGTKE 361

RESULT 10
 Sequence 2, Application US/08457997B
 Patent No. 5766508
 CURRENT APPLICATION NUMBER: 6
 APPLICANT: Kolattukudy, P. E.
 TITLE OF INVENTION: Otitis Media Vaccine
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calfee, Halter and Griswold
 STREET: Suite 1800 800 Superior Avenue
 CITY: Cleveland
 STATE: Ohio
 COUNTRY: U.S.A.
 ZIP: 44114-2688
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/467,722A
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gorlick, Mary B.
 REGISTRATION NUMBER: 34,329
 REFERENCE/DOCKET NUMBER: 22727/00102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (216) 622-8458
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-722A-2

Query Match 36.3%; Score 662.5; DB 2; Length 359;
 Best Local Similarity 43.3%; Pred. No. 1.8e-57;
 Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;

Query 1 MKAIFVLAAPKDNTWYAGKLGMQYHD---TGFYGNNGFQNNNGPTRNDQLAGAAGFG 56
 Db 13 LAAASVAAQAPQENTFYAGVKAGGSFHDGGINNNNGAIIKGKGLSSNNYGRNFTYGVFG 72

Query 57 YQV---NPyLGFEMGFDWLGRMAYKGSVDNGCAKQ---GVQLTAKLGYPITDLDIY 108
 Db 73 YQILNQDNGLAAELGYDFGRAKLR---EAGPKAKHTNNGAYSLKGSEYVLDGLDVY 129

Query 109 TRLGGMWRAIDSQKGNTASTGV---SRSEBDTGVSPVAGGVIEWAFTDIATLEYQMVNN 165
 Db 73 YQILNQDNGLAAELGYDFGRAKLR---EAGPKAKHTNNGAYSLKGSEYVLDGLDVY 129

Query 109 TRLGGMWRAIDSQKGNTASTGV---SRSEBDTGVSPVAGGVIEWAFTDIATLEYQMVNN 165
 Db 130 GRAGVALVRSYDKFYEDANGTRDHKGRTARASGLFAGVAYVLPLAVRLEYQMVTR 189

Query 166 IG-----DAGTVGTRPDNGMLSIGSYRFQGDAAPVVAAPAPAPAEVATKHFITLKD 218
 Db 190 VGYKRPQDKPNTAYNPWIIGCINAGISYRFQGCE-APVVA---APMVSKTFSLNSD 243

Query 219 VLFNFNKATLKPQEGQALDQLYTOLSNMPKDSAVVLYTDIGSEANQQLSERKAQS 278
 Db 244 VTFAGKANIKPQOQATLDSVYGEISQV---KSRKVAVAGYTRIGSDAFNVKLSQERADS 301

Query 279 VVDYLWAKGIPAGKISARGMGEISNPTGNTCDNVAKARALIDCLAPDRVEIYVGK 336
 Db 302 VANYFWAKGVAAADASATGYGEANPVIGATCDQVKRKALIACLAPDRVEIAVNGTK 359

RESULT 13
 US-09-665A-153
 : Sequence 153, Application US/09809665A
 : Patent No. 670050
 : GENERAL INFORMATION:
 : APPLICANT: Lowery, E., David, et al.
 : TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
 : FILE REFERENCE: 28341/00435
 : CURRENT FILING DATE: 2001-03-15
 : PRIORITY NUMBER: 69-115, 453
 : PRIORITY FILING DATE: 1999-09-10
 : PRIORITY NUMBER: 69-128, 689
 : PRIORITY FILING DATE: 1999-04-09
 : PRIORITY NUMBER: 09-545, 199
 : PRIORITY FILING DATE: 2000-04-06
 : NUMBER OF SEQ ID NOS: 197
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 153
 : LENGTH: 369
 : TYPE: PRT
 : ORGANISM: *Actinobacillus pleuropneumoniae*
 : US-09-809-665A-153

Query Match 35.5%; Score 646.5; DB 2; Length 369;

Best Local Similarity 41.1%; Pred. No. 7 46-56; Matches 153; Conservative 60; Mismatches 110; Indels 49; Gaps 12; Db 183 EYQYLNKAGNLNKLVRSGTQDVDFQYAPD1HSVTAGLSYRFQGAVAPVV----EPE 236

Qy 1 MKAIFVLNAPKONTWYAGKLGNSOYHTGFGY-NGFQNNNGPTRNDQ----L 49
Db 11 LSAAAVAAQAPQNTFYAGKVGSSFH---HCVNQKJSGHDDRYNTRKYGINRNSV 66

Qy 50 GAGAGGGYCV---NPYLGFMGKDWLGRMAYKGKSVNDGAFK---AQGVOLTAKLGYP 100
Db 67 TYGVFGGYQIQLNQNNGFGLAELGYDYYGRV--RGNDE - FRVTKHSAGLNALKPSY 122

Qy 101 ITDDLDIYTRLGGMWRADSKGNVASTGVSRSE --HDGVSPVFAGGVWAWTRDIATR 157
Db 123 VLPDLDVYKGVGIAVRNQYK-YGAENTNESTTKFHKLKASTLIGAGYEALPELAR 181

Qy 158 LEYQVNNICDAGTY---GTR-----PDNGMLSLGYSYRFQEDAAPVWAPAPAP 206
Db 182 VEYQYLNKAGNLNKLVRSGTQDVDFQYAPD1HSVTAGLSYRFQGAVAPVV----BP 235

RESULT 15
US-09-506-078-46
; Sequence 46, Application US/09506078

Qy 207 EVATKHFHTLKSVDLFNPKNATLKEPGQQQLDOLYQTLNSMDPKGSAYVLTGVTDRIGSEA 266
Db 236 EVVTKNFASSSDVLFDFGKSLPKPAATLDAANTEIANGLATPAIQNGYTRIGSEA 295

Qy 267 YNQOLSEKRAQSVYDYLVARGIPAKISARGMGSNPVIGNTCDNVKARAALIDCLAPDR 326
Db 296 SNLKLQSQRRAETVANYLVSKGQNPAVTAVGYGEANPVTGATCDVKGRKALIACLAPDR 355

Qy 327 RVELEVKGYKEV 338
Db 356 RVEVQVQGAKNV 367

RESULT 14
US-09-418-980-10
; Sequence 10, Application US/09418980

; Patent No. 6713071
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarsch, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankenbauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
; FILE REFERENCE: PC954A
; CURRENT APPLICATION NUMBER: US/09/418, 980
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO: 10
; LENGTH: 369
; TYPE: PRF
; ORGANISM: Actinobacillus pleuropneumoniae
; US-09-418-980-10

Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3 7e-55; Mismatches 60; Indels 47; Gaps 11; Db 123 VLPDLDVYKGVGIAVRNQYGAENTNESTTKFHKLKASTLIGAGYEALPELARV 182

Qy 1 MKAIFVLNAPKONTWYAGKLGNSOYHTGFGY-NGFQNNNGPTRNDQ----L 49
Db 11 LSAAAVAAQAPQNTFYAGKVGSSFH---HCVNQKJSGHDDRYNTRKYGINRNSV 66

Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3 7e-55; Mismatches 60; Indels 47; Gaps 11; Db 123 VLPDLDVYKGVGIAVRNQYGAENTNESTTKFHKLKASTLIGAGYEALPELARV 182

Qy 50 GAGAGGGYCV---NPYLGFMGKDWLGRMAYKGKSVNDGAFK---AQGVOLTAKLGYP 100
Db 67 TYGVFGGYQIQLNQNNGFGLAELGYDYYGRV--RG-NDGEFRAMKHSAGLNALKPSY 122

Qy 101 ITDDLDIYTRLGGMWRADSKGNVASTGVSRSE --HDGVSPVFAGGVWAWTRDIATR 158
Db 123 VLPDLDVYKGVGIAVRNQYK-YGAENTNESTTKFHKLKASTLIGAGYEALPELAR 182

Qy 159 EYQVNNICDAGTY---GTR-----PDNGMLSLGYSYRFQEDAAPVWAPAPAP 207
Db 183 EYQYLNKAGNLNKLVRSGTQDVDFQYAPD1HSVTAGLSYRFQGAVAPVV----EPE 236

Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3 7e-55; Mismatches 60; Indels 47; Gaps 11; Db 123 VLPDLDVYKGVGIAVRNQYGAENTNESTTKFHKLKASTLIGAGYEALPELARV 182

Qy 1 MKAIFVLNAPKONTWYAGKLGNSOYHTGFGY-NGFQNNNGPTRNDQ----L 49
Db 11 LSAAAVAAQAPQNTFYAGKVGSSFH---HCVNQKJSGHDDRYNTRKYGINRNSV 66

Qy 50 GAGAGGGYCV---NPYLGFMGKDWLGRMAYKGKSVNDGAFK---AQGVOLTAKLGYP 100
Db 67 TYGVFGGYQIQLNQNNGFGLAELGYDYYGRV--RG-NDGEFRAMKHSAGLNALKPSY 122

Qy 101 ITDDLDIYTRLGGMWRADSKGNVASTGVSRSE --HDGVSPVFAGGVWAWTRDIATR 158
Db 123 VLPDLDVYKGVGIAVRNQYK-YGAENTNESTTKFHKLKASTLIGAGYEALPELAR 182

Qy 159 EYQVNNICDAGTY---GTR-----PDNGMLSLGYSYRFQEDAAPVWAPAPAP 207
Db 183 EYQYLNKAGNLNKLVRSGTQDVDFQYAPD1HSVTAGLSYRFQGAVAPVV----EPE 236

Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3 7e-55; Mismatches 60; Indels 47; Gaps 11; Db 123 VLPDLDVYKGVGIAVRNQYGAENTNESTTKFHKLKASTLIGAGYEALPELARV 182

Qy 1 MKAIFVLNAPKONTWYAGKLGNSOYHTGFGY-NGFQNNNGPTRNDQ----L 49
Db 11 LSAAAVAAQAPQNTFYAGKVGSSFH---HCVNQKJSGHDDRYNTRKYGINRNSV 66

Qy 50 GAGAGGGYCV---NPYLGFMGKDWLGRMAYKGKSVNDGAFK---AQGVOLTAKLGYP 100
Db 67 TYGVFGGYQIQLNQNNGFGLAELGYDYYGRV--RG-NDGEFRAMKHSAGLNALKPSY 122

Qy 101 ITDDLDIYTRLGGMWRADSKGNVASTGVSRSE --HDGVSPVFAGGVWAWTRDIATR 158
Db 123 VLPDLDVYKGVGIAVRNQYK-YGAENTNESTTKFHKLKASTLIGAGYEALPELAR 182

Qy 159 EYQVNNICDAGTY---GTR-----PDNGMLSLGYSYRFQEDAAPVWAPAPAP 207
Db 183 EYQYLNKAGNLNKLVRSGTQDVDFQYAPD1HSVTAGLSYRFQGAVAPVV----EPE 236

Search completed: November 26, 2005, 00:20:50
Job time : 48 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please, note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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DR	InterPro; IPR000498; OmpA_tmem.
PFAM	PF00691; OmpA; 1.
DR	PFAM; PF01389; OmpA; membrane; 1.
PRINTS	PRO1021; OmpA_DOMAIN.
DR	PRINTS; PRO1022; OUTMEMBRANA.
DR	PRODOM; PD00930; OmpA/MotB; 1.
PROSITE	PS01068; OMPA; 1; 1.
DR	PROSITE; PS55123; OMPA; 2; 1.
KW	Conjugation; Ion transport; Membrane; Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
KW	Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
FT SIGNAL	1 ? Potential.
FT CHAIN	?
FT TRANSMEM	344 Outer membrane protein A.
FT TRANSMEM	15 Potential.
FT TRANSMEM	48 Potential.
FT TRANSMEM	63 Potential.
FT TRANSMEM	78 Potential.
FT TRANSMEM	90 Potential..
FT TRANSMEM	104 Potential.
FT TRANSMEM	119 Potential.
FT TRANSMEM	140 Potential.
FT TRANSMEM	151 Potential.
FT TRANSMEM	157 Potential..
FT TRANSMEM	173 Potential..
FT TRANSMEM	179 Potential..
FT REPEAT	199 Potential.
FT REPEAT	200 Potential.
FT REPEAT	201 2.
FT REPEAT	203 204 3.
FT REPEAT	205 206 4.
FT DOMAIN	208 336 OmpA-like.
FT REGION	209 206 4 X 2 AA tandem repeats of A-P.
FT DISULFID	309 321 By disulfide.
FT CONFLICT	335 335 Y -> I (in Ref. 2).
SQ SEQUENCE	344 AA; 37061 MW; AC88AAE3 B7871B16 CRC64;
Query Match	99.5% Score 1813; DB 1; Length 344;
Best Local Similarity	100.0% Pred. No. 7.6e-131; Indels 0; Gaps 0;
Matches	342; Conservative 0; Mismatches 0;
Qy	1 MKAIFVLAAPKONTWYAGGKLGLSQQYHDTGFYCNGFQNNNGPRNDLGAGAFCGGYQVN 60
Db	1 MKAIFVLAAPKONTWYAGGKLGLSQQYHDTGFYCNGFQNNNGPRNDLGAGAFCGGYQVN 60
Qy	61 PYLGFEMGYDWLGRMAYKGSVDNGAFAKQGVQLTAKLGYPITDDLDITRLGGMWRADS 120
Db	61 PYLGFEMGYDWLGRMAYKGSVDNGAFAKQGVQLTAKLGYPITDDLDITRLGGMWRADS 120
Qy	121 KGNYASTGVSREHDGTGSPVAGGQEVWATRDIATRLEYQWNINIDAGTGTRPDNGM 180
Db	121 KGNYASTGVSREHDGTGSPVAGGQEVWATRDIATRLEYQWNINIDAGTGTRPDNGM 180
Qy	181 LSLGVSYRFQEDAAPVYAAPAPAPAEVATKHFTLKSDVLFENPKATLKPEQGQALDQY 240
Db	181 LSLGVSYRFQEDAAPVYAAPAPAPAEVATKHFTLKSDVLFENPKATLKPEQGQALDQY 240
Qy	241 TQLSNMDPKDGSAVVLYGTYDRIGSEAYNQQLSERAQSVYDLYVAKGIPAKLSARGNGE 300
Db	241 TQLSNMDPKDGSAVVLYGTYDRIGSEAYNQQLSERAQSVYDLYVAKGIPAKLSARGNGE 300
Qy	301 SNPVTGNTCDNVKARAALIDCLADDRYIEVKGKYEVVTQP 342
Db	301 SNPVTGNTCDNVKARAALIDCLADDRYIEVKGKYEVVTQP 342
RESULT 2	OMPA_ENTAE STANDARD; PRT; 350 AA.
ID	OMPA_ENTAE
AC	PO9146;
DT	01-MAR-1989 (Rel. 10, Created)
DT	01-MAR-1989 (Rel. 10, Last sequence update)
DE	Outer membrane protein A precursor.
GN	Name=ompA;
OS	Enterobacter aerogenes (Aerobacter aerogenes).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Enterobacter.
NCBI_TAXID	548;
OX	
RN	
Query Match	84.6% Score 1542; DB 1; Length 350;
Best Local Similarity	87.5% Pred. No. 5e-110; Indels 6; Gaps 2;
Matches	295; Conservative 10; Mismatches 26;
Qy	6 VLNAAPKDNTWYAGGKLGLSQQYHDTGFYCNGFQNNNGPRNDLGAGAFCGGYQVNPLGF 65
Db	13 VAQAPKDNTWYAGGKLGLSQQHDTGFYCNGFQNNNGPRNDLGAGAFCGGYQVNPLGF 66
Qy	77 EMG7DWLGRMAYKGSVDNGAFAKQGVQLTAKLGYPITDDLDITRLGGMWRADSCKGNYA 125
Db	77 EMG7DWLGRMAYKGSVDNGAFAKQGVQLTAKLGYPITDDLDITRLGGMWRADSCKGNYA 126
Qy	126 STGVSREHDTGSPVAGGQEVWATRDIATRLEYQWNIDAGTGTRPDNGMSLGV 18;

Db 132 SNSIAGDNHDTGVSPVFAGGVWENAMTRDIATRLEYQWYNNINGDAGTVVRPDNGMLSVGV 191
 Qy 186 SYRQGQDAPVWVAPAPAPEAVTKHFTLKSVDLFNFNKATLKPEGQALDOLYTQLSN 245
 Db 192 SYRQGQDAPVWVAPAPAPEAVTKHFTLKSVDLFNFNKATLKPEGQALDOLYTQLSN 251
 Qy 246 MDPKDGSATVLGTYDRIGSEAYNQOLSEKRAQSTVDLYAKGIPAGKISARGNGESNFT 305
 Db 252 MDPKDGSATVLGTYDRIGSEAYNQOLSEKRAQSTVDLYAKGIPAGKISARGNGESDFT 311
 Qy 306 GNTCDNVKVRARAALIDCLADPDRVIEVKYKEYVTTQ 342
 Qy 312 GNTCDNVKVRARAALIDCLADPDRVIEVKYKDVTQ 348

RESULT 3
 Q[REDACTED] SHIDY STANDARD; PRT; 351 AA.
 AC P02935;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Outer membrane protein A precursor (Outer membrane protein II).
 Name=ompA;
 GN Shigella dysenteriae.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigellales.
 OX NCBI_TaxID=622;
 RN [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE:82221414; PubMed=6283478;
 RX Braun G., Cole S.T.;
 RA RT "The nucleotide sequence coding for major outer membrane protein OmpA of Shigella dysenteriae.";
 RL Nucleic Acids Res 10:2367-2378 (1982).
 CC -I- FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phage. Also acts as a porin with low permeability that allows slow penetration of small solutes (By similarity).
 CC -I- SUBUNIT: Monomer (Probable).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -I- SIMILARITY: Belongs to the ompA family.
 CC -I- SIMILARITY: Contains 1 OmpA-like domain.

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EMBL; V01344; CAA4638.1; -; Genomic_DNA.
 DR; PIR; A0435; MNEBD.
 HSSP; P02934; 1QPF.
 DR; P02935; 22-2C2; InterPro; IPR00664; Bac_OmpA.
 DR; P01022; OMpadomaine; P01021; OMpadomaine; 1.
 DR; InterPro; IPR006655; OmpA/MctB.
 DR; InterPro; IPR006650; OmpA_Like.
 DR; PFM; PF00691; OmpA; 1.
 DR; PFM; PF01380; OmpA_mtmem.
 DR; PRINTS; PRO1022; OUTRMBRANE.
 DR; PRODOM; PD000930; OmpA/MotB; 1.
 DR; PROSITE; PS01068; OMPA; 1.
 DR; PROSITE; PS51123; OMPA; 2.
 DR; Conjugation; Ion_transport; Membrane; Outer_membranes; Transport; Phage_recognition; Porin; Repeat; Signal; Transmembrane; Transport.
 KW SIGNAL 1 21
 FT SIGNAL 1 21
 FT CHAIN 22 351
 FT TRANSMEM 27 40
 FT TRANSMEM 55 67

Db 70 85
 FT TRANSMEM 97 107
 FT TRANSMEM 111 126
 FT TRANSMEM 147 158
 FT TRANSMEM 164 180
 FT TRANSMEM 186 197
 FT REPEAT 206 207
 FT REPEAT 208 209
 FT REPEAT 210 211
 FT REPEAT 212 213
 FT DOMAIN 215 213
 FT REGION 206 213
 FT DISULFID 316 328
 SQ SEQUENCE 351 AA; 37741 MW; 1499AA5F5395B335B CRC64;

Query Match 83.7%; Score 1525.5; DB 1; Length 351;
 Best Local Similarity 84.6%; Pred. No. 9.3e-109; Pdb. No. 9.3e-109;
 Matches 20; Mismatches 27; Indels 5; Gaps 1;

Qy 6 VLNAAPKDNTWYAGGLKGWSQYHDTGFYNGFQNNNGPTRNDLGAGAFGGYQVNPNYLG 65
 Db 18 VAQAAPKDNTWYTGAKLKGWSQYHDTGF1----DNGTGTENHNLQGAGAFGGYQVNPNYGF 72
 Qy 66 EMQYDWLGRMAYKGSVNGAFKAQGVQLTAKLGYPITDDOLYTTRLGEMWRAADSCKNYA 125
 Db 73 EMQYDWLGRMYPKGSVNGENGAQGVQLTAKLGYPITDDLVTRLGEMWRAADSCKNYA 132
 Qy 126 STCVSRSEHDTGVSPVFAGGVWAVTRIATRLEYQVNINIGDAGTVTRPDNGMLSLGV 185
 Db 133 VTCBSEKHNHDGTGVSPVFAGGVWAVTRIATRLEYQVNINIGDAGTVTRPDNGLSLGV 192
 Qy 186 SYRFGQDAAPIVYAPAPAPAEVATKPTLKSDFLNFKATLKPEQGAOLDLYTQLSN 245
 Db 193 SYRFGQDAAPIVYAPAPAPAEVATKPTLKSDFLNFKATLKPEQGAOLDLYTQLSN 252
 Qy 246 MDPKDGSAVLVGLGYTRIGSEAYNQOLSEKRAQSVVYDYLVAKGIPAGKISARGNGESNPV 305
 Db 253 LDPKDGSUVVGLGYTRIGSDAYNQLSERRASQSVVYDYLISKGIPADKISARGNGESNPV 312
 Qy 306 GNTCDNVKARAALIDCLAPDRVEIEVKYKEVVTQP 342
 Db 313 GNTCDNVKARAALIDCLAPDRVEIEVKYKEVVTQP 349

RESULT 4

Q[REDACTED] ENTSA_ID Q52JK5; ENTSA PRELIMINARY; PRT; 347 AA.
 AC Q52JK5;
 DT 13-SEP-2005 (TREMBLref; 31, Created)
 DT 13-SEP-2005 (TREMBLref; 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLref; 31, Last annotation update)

OS Enterobacter sakazakii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OC NCBI_TaxID=28141;
 RN [1] Nucleotide sequence of OmpA from Enterobacter sakazakii in Infant Formula.;
 RN STRAIN=ATCC 51329;
 RN Mohan Nair M.K., Venkitanarayanan K.S.;
 RN "Cloning and Sequencing of the Major Outer Membrane Protein Gene OmpA and Development of A Specific PCR for Rapid Detection of Enterobacter sakazakii in Infant Formula.";
 RN Submitted (APR-2005) to EMBL/GenBank/DDBJ databases.
 RL DR EMBL; DQ000206; AAY18798.1; -; Genomic DNA.
 SEQUENCE 347 AA; 37054 MW; 84DB8148F5395B335B CRC64;

Query Match 83.0%; Score 1513.5; DB 2; Length 347;
 Best Local Similarity 84.9%; Pred. No. 7.7e-108; Pdb. No. 7.7e-108;
 Matches 287; Mismatches 16; Indels 24; Gaps 3;

Qy 6 VLNAAPKDNTWYAGGLKGWSQYHDTGFYNGFQNNNGPTRNDLGAGAFGGYQVNPNYLG 65

18	VAQAPKDNNTWYAGG3KLGWSQFHDTSFI-----	PNGPTHESQLGAGAFCGGYQVNPNVGF	72
66	EMGYDYLGRMAYKGSYDNGAFAQGYVOLTAKIGYPTTDDLDIYTTRLGMMWYRADSCKNYA	125	
73	EMGYDYLGRMAYKGSYDNGAFAQGYVOLTAKIGYPTTDDLDIYTTRLGMMWYRADSCKNYA	132	
126	STGVSRSEHDGTGVSPVFAGGYEWATRDIATRLEYQVNNGDAGTGTGTRPDNGMLSLGV	185	
133	G-----DDHDGTGVSPVFAGGYEWATRDIATRLEYQVNNGDAGTGTGTRPDNGMLSLGV	187	
186	SYRFGQEDAPVVAAP	244	
188	SYRFGQEDAPVVAAP	247	
245	NMDPKDGSAVVLGYTDRIGSAYNQOQSERQAQSVDYLVARGIPACKISARGMGEESNPV	304	
248	NLDPKDGSUVVLFTRIGSDAYNQGSERQAQSVDYLISKGTPNSKISARGMGEESNPV	307	
305	TGNTCDVNKARAALIDCLAPDRRVELEVKGKYKEVYTOP	342	
308	TGNTCDVNKARAALIDCLGPDRRVELEVKGKYKEVYTOP	345	

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STMDN-0157:NY / Saccharomyces cerevisiae / STMDN-05000052 / EUEC.

MEDLINE=21156231; PubMed=11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii A

na, C.-G., Otsuji S., Nakayama K., Murata I., Iida T., Takami H., Honda T., Sasabawara N., Ogasawara N., Yasunaga T., Kubara S., Shiba T., Uwatori M., Shinagawa H.

"Complete genome sequence of *enterohemorrhagic Escherichia coli* O157:H7".

DNA Res. 8:11-22 (2001).

stabilization required for the action of coagulants and the formation of aggregates in conjunction. Serves as a

receptor for a number of T-even like phages. Also, action of small amounts of saponin generates slow lysis.

solute (By similarity).
concentrated

-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane

- !- SIMILARITY: Belongs to the *ompA* family.
- !- SIMILARITY: Contains 1 *OmpA*-like domain.

the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

SIGNAL	1	21	By similarity.
CHAIN	22	346	Outer membrane protein A.
TOPO DOM	22	28	Periplasmic (By similarity).
TRANSEMM	27	37	By similarity.
TOPO DOM	38	54	Extracellular (By similarity).
TRANSEMM	55	66	By similarity.
TOPO DOM	67	69	Periplasmic (By similarity).
TRANSEMM	70	78	By similarity.
TOPO DOM	79	95	Extracellular (By similarity).
TRANSEMM	96	107	By similarity.
TOPO DOM	108	111	Periplasmic (By similarity).
TRANSEMM	112	124	By similarity.
TOPO DOM	125	137	Extracellular (By similarity).
TRANSEMM	138	151	By similarity.
TOPO DOM	152	155	Periplasmic (By similarity).
TRANSEMM	156	163	By similarity.
TOPO DOM	164	181	Extracellular (By similarity).
TRANSEMM	182	190	By similarity.
TOPO DOM	191	246	Periplasmic (By similarity).
REPEAT	201	202	1.
REPEAT	203	204	2.
REPEAT	205	206	3.
REPEAT	207	208	4.
DOMAIN	210	338	OmpA-like.
REGION	197	308	Binge-like.
REGION	208	400	4 X 2 AA tandem repeats of A-P.

Position	Mutant		Control	
	AA	AA	AA	AA
6	V	I	A	A
14	D	D	D	D
203	C	C	C	C

66 ENGYDWIGRMA YKGVSIDNGA FKAQGVOLTAKUGPYITDLDIYTRLGGMWRADSKGNYA 125

73	ENGDWIGRMPYKGSVNGAYAQQVQJIAKJYPTIDLUJYTRLGKVNRAJIKSN--	130
74	STGVRSSEBDTGYSPVAGGVEMAVTDIATLREYQNTNNIGDAGTVTRPDNGMLSLGV	185

131 --VYGNHDTGSPVFGGVEAYITPEIATRLEYQWTNNNGDAHTIGTRPDNGMLSLGV 187

Db	248	LDPKDGsvvvVLLGTYDRIGSDAYNQGLSERRAQSVDYLKGTPADKTSARGMGESENPT	307	RT "Comparing the predicted and observed properties of proteins encoded in the genome of <i>Escherichia coli</i> K-12.";
Qy	306	GNTCDNVKRAALIDCLADPDRVTEVKRYKEVVTQ	342	RT Electrophoresis 18:1259-1313 (1997).
Db	308	GNTCDNVKRAALIDCLADPDRVTEVKGIKDVVTQ	344	RL [7] PROTEIN SEQUENCE OF 22-32.
				RC STRAIN=K12 / W3110;
RESULT 6				RA Molloy M.P.; Herbert B.R.; Walsh B.J.; Tyler M.I.; Traini M.,
OMPA_ECOLI				RA Sanchez J.-C.; Sanchez J.-C.; Ravier F.; Golaz O.; Hughes G.J.,
ID _OMPA_ECOLI STANDARD		PRT; 346 AA.		RA Frutiger S.; Daquet N.; Wilkins M.; Appel R.D.; Bairoch A.,
AC P0A910; P02924;				RA Hochstrasser D.F.; Submitted (SEP-1994) to Swiss-Prot.
DT 21-JUL-1986 (Rel. 01, Created)				RL [8] RN [8]
DT 21-JUL-1986 (Rel. 01, Last sequence update)				RP PROTEIN SEQUENCE OF 22-26.
DT 13-SEP-2005 (Rel. 48, Last annotation update)				RC STRAIN=K12 / W3110;
DE Outer membrane protein A precursor (Outer membrane protein III).				RA MEDLINE=98291876; PubMed=9629924;
CA Name=ompA; Synonyms=con, tolg, tut; OrderedLocusName=b0957;				RA Molloy M.P.; Herbert B.R.; Walsh B.J.; Tyler M.I.; Traini M.,
OC Escherichia coli.				RA Sanchez J.-C.; Hochstrasser D.F.; Williams K.L.; Gooley A.A.,
OC Bacteriophage; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				RA "Extraction of membrane proteins by differential solubilization for separation using two-dimensional gel electrophoresis.";
OC Enterobacteriaceae; Escherichia.				RA Electrophoresis 19:837-844 (1998).
OX NCBI_TaxID=562;				RL [9] RN [9]
RP MUTANTS RESISTANT TO PHAGE ENTRY.				RP MUTANTS RESISTANT TO PHAGE ENTRY.
RC MEDLINE=8424337; PubMed=6086577;				RX MEDLINE=86033606; PubMed=3502787;
RC "Escherichia coli K-12 outer membrane protein (OmpA) as a bacteriophage receptor: analysis of mutant genes expressing altered proteins.";				RA Morona R.; Klose M.; Henning U.,
RA Beck E.; Bremer E.;				RA Morona R.; Kramer C.; Henning U.,
RT "Nucleotide sequence of the gene <i>ompA</i> coding the outer membrane protein II of <i>Escherichia coli</i> K-12.";				RT RT RT RT
RT Nucleic Acids Res. 8:3011-3024 (1980).				RT Bacteriolog. 159:570-578 (1984).
RL RN [10]				RL J. Bacteriol. 164:539-543 (1985).
RC NUCLEOTIDE SEQUENCE.				RP MUTANTS RESISTANT TO PHAGE ENTRY.
RC STRAIN=K12;				RP MEDLINE=92129334; PubMed=1370823;
RC MEDLINE=811053729; PubMed=6253901;				RC STRAIN=K12;
RA Beck E.; Bremer E.;				RA Sugawara E.; Nikaido H.,
RT "Nucleotide sequence of the gene <i>ompA</i> coding the outer membrane protein II of <i>Escherichia coli</i> K-12.";				RT "Pore-forming activity of OmpA protein of <i>Escherichia coli</i> .";
RT Nucleic Acids Res. 8:3011-3024 (1980).				RT J. Biol. Chem. 267:2507-2511 (1992).
RL RN [11]				RA Kuhn A.; Kieber D.; Koehne C.; Zhu H.-Y.; Tschantz W.R.; Dalbey R.B.,
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				RA "Evidence for a loop-like insertion mechanism of pro-Omp A into the
RC STRAIN=K12;				RA inner membrane of <i>Escherichia coli</i> .";
RC MEDLINE=97061202; PubMed=8905232;				RL Eur. J. Biochem. 226:891-897 (1994).
RA Obshima T.; Aliba H.; Baba T.; Fujita K.; Hayashi K.; Honjo A.,				RN [12] RN [12]
RA Ikemoto K.; Inada T.; Itoh T.; Kajihara M.; Kanai K.; Kashimoto K.,				RP SUBCELLULAR LOCATION.
RA Kimura S.; Kitagawa M.; Makino T.; Maeda S.; Miki T.; Mizobuchi K.,				RA MEDLINE=7813480;
RA Mori H.; Motomura K.; Nakamura Y.; Nishimoto K.; Saito N.,				RA Kuhn A.; Kieber D.; Koehne C.; Zhu H.-Y.; Tschantz W.R.; Dalbey R.B.,
RA Sanpei K.; Seki Y.; Tagami H.; Takemoto K.; Wada C.; Yamamoto Y.,				RA "Evidence for a loop-like insertion mechanism of pro-Omp A into the
RA Yano M.; Horuchi T.,				RA inner membrane of <i>Escherichia coli</i> .";
RA RT A 718-rb DNA sequence of the <i>Escherichia coli</i> K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";				RL Eur. J. Biochem. 226:891-897 (1994).
RT RN [13]				RN [13]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				RP TOPOLOGY.
RC STRAIN=K12;				RX MEDLINE=94148615; PubMed=8106193;
RC MEDLINE=97061202; PubMed=8905232;				RA Gromiha M.M.; Ponnusamy P.K.,
RA Obshima T.; Aliba H.; Baba T.; Fujita K.; Hayashi K.; Honjo A.,				RT "Prediction of transmembrane beta-strands from hydrophobic
RA Blattner F.R.; Blunkett G. III.; Bloch C.A.; Perna N.T.; Burland V.,				RT characteristics of proteins.";
RA Riley M.; Collado-Vides J.; Glasner J.D.; Rode C.K.; Mayhew G.P.,				RA Int. J. Pept. Protein Res. 42:420-431 (1993).
RA Gregor J.; Davis N.W.; Kirkpatrick H.A.; Goeden M.A.; Rose D.J.,				RA RN [14]
RA Mau B.; Shao Y.,				RP TOPOLOGY.
RA RT "The complete genome sequence of <i>Escherichia coli</i> K-12.";				RA MEDLINE=99236577; PubMed=10368142;
RL RN [15]				RA RT "Structural and functional roles of the surface-exposed loops of the
RC PROTEIN SEQUENCE OF 22-346.				RL beta-barrel membrane protein OmpA from <i>Escherichia coli</i> .";
RC MEDLINE=81054820; PubMed=7001461;				RL RN [15] RN [15]
RA Chen R.; Schmidmayr W.; Kramer C.; Chen-Schmeisser U.; Henning U.,				RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 22-192.
RA "Primary structure of major outer membrane protein II (ompA protein of <i>Escherichia coli</i> K-12.";				RX MEDLINE=90023200; PubMed=9808047;
RT Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596 (1990).				RA Paulsch A.; Schulz G.E.,
RN [6]				RA "Structure of the outer membrane protein A transmembrane domain.";
RP PROTEIN SEQUENCE OF 22-34.				RT RT "High-resolution structure of the OmpA membrane domain.";
RC MEDLINE=811053729; PubMed=6253901;				RA Link A.J.; Robison K.; Church G.M.,
RA Paulsch A.; Schulz G.E.;				RA "High-resolution structure of the OmpA membrane domain.";

Qy	126	STGVSRSEHTDTGSVPVAGGEWAVTRDATTTRLEYQWNNINGDAGTGVPRPDNGMLSLGV	185	Db	131	--VYGNKHDTGVPVAGGEWAVTRDATTTRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187	Db	131	--VYGNKHDTGVPVAGGEWAVTRDATTTRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187	Db	131	--VYGNKHDTGVPVAGGEWAVTRDATTTRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187	Db	131	--VYGNKHDTGVPVAGGEWAVTRDATTTRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187
Qy	186	SYRGQEDAAPVVAAPAPAPEVATKHTFLKSVDLFNFNKATLKPEQOALDQLYTQLSN	245	Db	188	SYRGQEDAAPVVAAPAPAPEVATKHTFLKSVDLFNFNKATLKPEQOALDQLYTQLSN	245	Db	188	SYRGQEDAAPVVAAPAPAPEVATKHTFLKSVDLFNFNKATLKPEQOALDQLYTQLSN	245	Db	188	SYRGQEDAAPVVAAPAPAPEVATKHTFLKSVDLFNFNKATLKPEQOALDQLYTQLSN	245	Db	188	SYRGQEDAAPVVAAPAPAPEVATKHTFLKSVDLFNFNKATLKPEQOALDQLYTQLSN	245
Qy	246	MDPKDGSATVLTGTDIGSEAYNQOLSEKRAQSUVYDLYAKGIPAKISARGMGESENPT	305	Db	248	LDPKDGSVWLGTDIGSDAYNQLSERRAQSUVYDLYISKGIPAKISARGMGESENPT	307	Db	248	LDPKDGSVWLGTDIGSDAYNQLSERRAQSUVYDLYISKGIPAKISARGMGESENPT	307	Db	248	LDPKDGSVWLGTDIGSDAYNQLSERRAQSUVYDLYISKGIPAKISARGMGESENPT	307	Db	248	LDPKDGSVWLGTDIGSDAYNQLSERRAQSUVYDLYISKGIPAKISARGMGESENPT	307
Qy	306	GNTCDNVKARAAALDCLADPDRVTEIEVKGYKEVNTQP	342	Db	308	GNTCDNVKARAAALDCLADPDRVTEIEVKGYKEVNTQP	342	Db	308	GNTCDNVKARAAALDCLADPDRVTEIEVKGYKEVNTQP	342	Db	308	GNTCDNVKARAAALDCLADPDRVTEIEVKGYKEVNTQP	342	Db	308	GNTCDNVKARAAALDCLADPDRVTEIEVKGYKEVNTQP	342
RESULT 9																			
Q9L6J0_ECOLI																			
ID	Q9L6J0	ECOLI	PRELIMINARY;	PRT;	346	AA.													
AC	Q6PNM6	SHIBO	PRELIMINARY;	PRT;	346	AA.													
DT	05-JUL-2004	(TREMBLrel.	27, Created)	DT	01-OCT-2000	(TREMBLrel.	15, Created)												
DT	05-JUL-2004	(TREMBLrel.	27, Last sequence update)	DT	01-OCT-2000	(TREMBLrel.	15, Last sequence update)												
DT	05-JUL-2004	(TREMBLrel.	27, Last annotation update)	DT	01-MAR-2004	(TREMBLrel.	26, Last annotation update)												
DE	Outer membrane protein A precursor.																		
GN	Name=ompA;																		
OS	Shigella boydii.																		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;																		
OC	Enterobacteriaceae; Shigellaceae;																		
OX	NCBI_TaxID=562;																		
RN	RN																		
RP	RP																		
RC	RC																		
STRAIN	STRAIN=MalaysiaB631;																		
RA	RA																		
NIK	NIK Noorul Shakira M.S., Kirpal-Kaur B.S., Ravichandran M., Asma I., Mohd Zaki S.																		
RT	RT "Shigella boydii" Outer membrane protein A precursor (ompA) gene.;																		
RL	RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.																		
RA	RA "Shigella boydii" Outer membrane protein A precursor (ompA) gene.;																		
RT	RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.																		
DR	DR SMR; Q6PNM6; 22-1977.																		
DR	DR GO; GO:0016031; C:integral to membrane (sensu Gram-negative Bacteria); GO; GO:009219; C:outer membrane (sensu Gram-negative Bacteria); IEA.																		
DR	DR GO; GO:009219; C:outer membrane (sensu Gram-negative Bacteria); IEA.																		
DR	DR GO; GO:00598; P:structural molecule activity; IEA.																		
DR	DR InterPro; IPR01028; Bac_OmpA.																		
DR	DR InterPro; IPR01035; MotY.																		
DR	DR InterPro; IPR02368; OmpA.																		
DR	DR InterPro; IPR02368; OMPA/MotB.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro; IPR06650; OMPA_LIKE.																		
DR	DR InterPro																		

Qy	246	MDPKDGSAVVLGYTRIGSFAYNQOLSEKRAQSYVDLYAKGIPAKKISARGMGSNPVT	305
Db	248	LDPKDGSVVLGYTRIGSFAYNQOLSEKRAQSYVDLYAKGIPAKKISARGMGSNPVT	307
Qy	306	GNTCDNVKARAALIDCLAPRRVEEVKGKKEYVYQP	342
Db	308	GNTCDNVKARAALIDCLAPDRRVEEVKGKKEYVYQP	344
RESULT 10			
Qy	Q57QT3	SALCH PRELIMINARY; PRT; 350 AA.	
Db	Q57QT3_		
AC	Q57QT3_		
DT	10-MAY-2005 (TREMBLrel. 30, Created)		
DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)		
DE	Putative hydrogenase, membrane component.		
GN	Name=ompA; OrderedlocusName=SC1022;		
OS	Salmonella cholerae-suis (Salmonella enterica).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Salmonella.		
NCBI_TAXID	591; [1]		
RE: NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=SC-B67';		
RX	PubMed=1578495;		
RA	Chiu, C.-H., Tang, P., Chu, C., Hu, S., Bao, Q., Yu, J., Chou, Y.-Y., Wang, H.-S., Lee, Y.-S.;		
RA	The genome sequence of <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> , a highly invasive and resistant zoonotic pathogen.		
RT	;		
RU	Nucleic Acids Res. 33:1690-1698 (2005).		
DR	EMBL: AB017220; AAJ64948.1; -; Genomic_DNA.		
KW	Complete genome.		
SQ	SEQUENCE 350 AA; 37491 MW; 7C3529A442E234FC CRC64; [REDACTED]		
Query Match 82.3%; Score 1501; DB 2; Length 350; Best Local Similarity 83.1%; Pred. No. 7.1e-107; Matches 280; Conservative 25; Mis matches 26; Indels 6; Gaps 2;			
Qy	6 VLNAPKONTWYAGKLGKMSQHOTGFGYNGFQNNNGPTRNDLGAGAFCGGYQYNPVLGF	65	
Db	18 VAQAAPKONTWYAGKLGKMSQHOTGFGI -----NDGPTHENQLGAGAFCGGYQYNPVG	72	
Qy	66 EMGYDWLGKMAYKGSVDNGAFAKQVQLTAKLGYPITDDIYTRLGGWWRADSGKNA	125	
Db	73 EMGYDWLGKMPYKGDDNNGAYKAQGVQLTAKLGYPITDDLVTRLGGWWRADTKSNVP	132	
Qy	126 STGVSRESDTGYSPVAGGQEVWATRDIATRLEYQWVNNGIDACTVGRTRPDNGMLSLGV	185	
Db	133 G-GPSTKDDTGYSPVAGGQEVWATRDIATRLEYQWVNNGIDACTVGRTRPDNGMLSLGV	191	
Qy	186 SYRGQEDAPVVAAP	245	
Db	192 SYRGQEQEAPVVAAP	251	
Qy	246 MDPKDGSAVVLGYTRIGSFAYNQOLSEKRAQSYVDLYAKGIPAKKISARGMGSNPVT	305	
Db	252 LDPKDGSVVLGYTRIGSFAYNQOLSEKRAQSYVDLYAKGIPAKKISARGMGSNPVT	311	
Qy	306 GNTCDNVKARAALIDCLAPRRVTEVKGKKEYVYQP	342	
Db	312 GNTCDNVKARAALIDCLAPDRRVEEVKGKKEYVYQP	348	
RESULT 11			
QSPGD5	SALPA		
ID	QSPGD5_SALPA PRELIMINARY;		
AC	QSPGD5;		
DT	01-FEB-2005 (TREMBLrel. 29, Created)		
DT	01-FEB-2005 (TREMBLrel. 29, Last sequence update)		
DT	01-FEB-2005 (TREMBLrel. 29, Last annotation update)		
DE	Outer membrane protein A.		

RA	Waterson R., Wilson R.K.;	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium	Qy	126 STGVSSEHDGTGVSPVAGGIEWAVTRDIATRLEYQVNNTGAGTGTGTRPDNGMLSRGV 185
RT	RT2."		Db	133 G-GPSTKHDGTGVSPVAGGIEWAVTRDIATRLEYQVNNTGAGTGTGTRPDNGMLSRGV 191
RL	Nature 413:852-856 (2001).			
-I-	FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (BY similarity).		Qy	186 SYRFQDAAPIVVAAPAPAPAPAVATKHTFLKPSQALDOLYTLNSN 245
CC	-I- SUBUNIT: Monomer (Probable).		Db	192 SYRFQDAAPIVVAAPAPAPAVATKHTFLKPSQALDOLYTLNSN 251
CC	-I- SIMILARITY: Belongs to the <i>ompA</i> family.			
CC	-I- SIMILARITY: Contains 1 <i>ompA</i> -like domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL: XG2006; CAA6037.1; -; Genomic DNA.			
DR	EMBL; AB008746; AL20003.1; -; Genomic_DNA.			
DR	PIR; A04436; MMDBAT.			
DR	HSRP; P02934; 1Q0P.			
DR	SNR; P09316; 2-201.			
DR	SG10263.			
DR	SG10263; <i>ompA</i> .			
InterPro	IPR006634; Bac_ <i>ompA</i> .			
DR	InterPro; IPR02338; <i>ompA</i> .			
DR	InterPro; IPR006635; <i>ompA/MotB</i> .			
DR	InterPro; IPR006630; <i>ompA_LIKE</i> .			
DR	InterPro; IPR00438; <i>ompA_trem</i> .			
PFam	PF00691; <i>ompA</i> .			
PFam	PF01389; <i>ompA</i> .			
DR	PRINTS; PR01021; <i>OMMADOMAIN</i> .			
DR	PR01022; <i>OUTERMEMBRANA</i> .			
PRD0M	PRD00930; <i>ompA/MotB</i> .			
DR	PROSITE; PS01068; <i>OMPA</i> ; 1.			
DR	PROSITE; PS01123; <i>OMPA</i> ; 2.			
KW	Complete proteome; Conjugation; Ion transport; Membrane; Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.			
KW	Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.			
SIGNAL	1			
FT	CHAIN 22 350			
FT	TRANSMEM 27 40			
FT	TRANSMEM 55 67			
FT	TRANSMEM 70 85			
FT	TRANSMEM 97 107			
FT	TRANSMEM 111 126			
FT	TRANSMEM 146 157			
FT	TRANSMEM 163 179			
FT	TRANSMEM 185 196			
FT	REPEAT 205 206			
FT	REPEAT 207 208			
FT	REPEAT 209 210			
FT	REPEAT 211 212			
FT	DOMAIN 214 342			
FT	REGION 205 212			
FT	DISULFID 315 327			
FT	CONFFLICT 1.14 1.14			
FT	CONFFLICT 247 S->I (in Ref. 1).			
SQ	SEQUENCE 350 AA; 37515 MW; B4AC52C8C5D54FE CRC64;			
Query Match	82.0%; Score 1495; DB 1; Length 350;			
Best Local Similarity	82.8%; Pred. No. 2e-106;			
Matches	279; Conservative 26; Mismatches 6; Gaps 2;			
6	VLNAPKONTWAGGKLGNSQYHDGTGVNGFQNNGPTRNDOLGAGA ^F GGYQVNPNVLF 65			
Qy	VLNAPKONTWAGGKLGNSQYHDGTGVNGFQNNGPTRNDOLGAGA ^F GGYQVNPNVLF 72			
Db	18 VLNAPKONTWAGGKLGNSQYHDGTGVNGFQNNGPTRNDOLGAGA ^F GGYQVNPNVLF 72			
6	EMGYDWLGKMGAYKGSVDNGAFAKGQVQVLTAKLGYPITDLDYTRLGMMWRAFDKGNYA 125			
Qy	EMGYDWLGKMGAYKGSVDNGAFAKGQVQVLTAKLGYPITDLDYTRLGMMWRAFDKGNYA 125			
Db	73 EMGYDWLGKMGAYKGSVDNGAFAKGQVQVLTAKLGYPITDLDYTRLGMMWRAFDKGNYA 125			

RESULT 15

Q83RX2 SHIFL PRELIMINARY; PRT; 348 AA.

AC Q83RX2; Q7UD17; Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DT Outer membrane protein 3a (II*;G,d). Name=ompA; OrderedLocusName=S1123; SF0957; OS Shigella flexneri. Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigellales. NCBI TaxID=23;

OX RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566; Job time : 232 secs

RX Jin Q., Yuan Z., Xu J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chan R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.; "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157."; RT Nucleic Acids Res. 30:4432-4441 (2002).

RX STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=222590274; PubMed=12704152; DOI=10.1128/IAI.71.5.2775-2786.2003; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of *Shigella flexneri* serotype 2a strain 2457T."; Infec. Immun. 71:2775-2786 (2003).

DR EMBL; AE005674; AAN42586.2; -; Genomic DNA.

DR EMBL; AE016881; AAP16471.1; -; Genomic DNA.

DR SMR; Q83RX2; 22-201.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0009379; C:outer membrane (sansu Gram-negative Bacteria); IEA.

DR InterPro; IPR000498; F:structural molecule activity; IEA.

DR InterPro; IPR002368; OmPa.

DR InterPro; IPR006655; OmPa/MotB.

DR InterPro; IPR006690; OmPa_LIKE.

DR InterPro; IPR000494; OmPa_tmem.

DR PFO0091; OmPa; 1.

DR PFO1389; OmPa membrane; 1.

DR PRINTER; PR01023; NAFLGMOTY.

DR PRINTS; PR01021; OMPADOMAIN.

DR PRINTS; PR01022; OUTRMBRANE.

DR ProdOm; PR000930; OmPa/MotB; 1.

DR PROSITE; PS01068; OmPa; 1.

KW Complete proteome.

SEQUENCE 348 AA; 37283 MW; 42623C67041D62F4 CRC64;

Query Match 80.8%; Score 1473; DB 2; Length 348;

Best Local Similarity 83.4%; Pred. No. 9; 9.e-10;

Matches 281; Conservative 18; Mismatches 30; Indels 8; Gaps 3;

Qy 6 VLNRAPKDNWYAGGKLGWSQYHDTGIFYNGNGPQNNGPTRNDLQAGAFAFGGYQVNPNYLG 65

Db 18 VAQAPKDNWYAGGKLGWSQYHDTGIFT----PNNGPTHENOLQAGAFAFGGYQVNPNYGF 72

Qy 66 EMGYDWLGRMAYKGSVDNGAFAQGVQVLTAKLGYPITDDIYTRLGGMWRAKSGKNA 125

Db 73 EMGYDWLGRMPTKGDNLNGAYKAQGVQVLTAKLGYPITDDIYTRLGGMWRAKANVP 132

Qy 126 STGVRSRSHDTGYSVPFAGGVEMAVTRDIAKTRLYQWNNNGDAGTVETRDNGMLSLGV 185

Db 133 G-GASFQHDHTGYSVPFAGGVETAPPIBIAKTRLYQWNNNGDAGTVETRDNGMLSLGV 191

Qy 186 SYRFGQEDAAPVYAPAPAPAEVATKHTFLKSDVLFNPKATLKPEQGAALDOLYSQLN 245

Db 192 SYRFGQEDAAPVY-APAPAPEVQKHTFLKSDVLFNPKATLKPEQGAALDOLYSQLN 249

Qy 246 MDPKDGSVAVLGLYTRDGSAYNQLSERQAQSVDYLVAKGIPAKISARGNGESNPVT 305

Db 250 LDPRDGSSVVLGLYTRDGSAYNQLSERQAQSVDYLVAKGIPAKISARGNGESNPVT 309

Qy 306 GNTCDNVRQRAALIDCLAPDRRVEIEVKGYKEYVTTQ 342

Db 310 GNTCDNVRQRAALIDCLAPDRRVEIEVKGYKEYVTTQ 342

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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:59:49 ; Search time 40 Seconds
827.464 Million cell updates/sec

Title: US-09-013-772A-2
Perfect score: 1823
Sequence: 1 MKAIFVTLNAAPKDNTWYAGG..... DRRVIEVKGYKEVTTQPG 344

Scoring table: BLOSUM32
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96226763 residues

Total number of hits satisfying chosen parameters: 283416

RESULT 1
JCG558
outer membrane protein A precursor - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 05-Dec-1998 #Sequence_revision 05-Dec-1998 #text_change 07-May-1999
C:Accession: JC6558
R:Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Baussian, T.; H:Gene 210, 93-101, 1998
A:Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation
A:Reference number: JC6558; MUID:98192544; PMID:9524233
A:Accession: JC6558
A:Molecule type: DNA
A:Residues: 1-356 <NGU>
A:Cross-References: UNIPARC:UPI00001780DF
A:Experimental source: IP I145
C:Genetics:
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-356/Product: outer membrane protein A #status predicted <SIG>

Query Match 97.8%; Score 1782; DB 2; Length 356;
Best Local Similarity 99.4%; Pred. No. 1e-127;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNQFNNNGPTRNDLQAGAGFGGYQVNPNYLG 65
Db 18 VAOAPKDNTWYAGGKLGWSQYHDTGFYGNQFNNNGPTRNDLQAGAGFGGYQVNPNYLG 77
Qy 66 EMQYDWLGRMAYGKSVNDNGAFAQGVOLTAKUGYPITDLDLYTRLGCMYWRADSKGNYA 125
Db 78 EMQYDWLGRMAYGKSVNDNGAFAQGVOLTAKUGYPITDLDLYTRLGCMYWRADSKGNYA 137
Qy 126 STGVYRSSEHDGTGSPVFAFGVEMATRDIATLEYQWVNNGDAGTGTTRPDNGMLSLGV 185
Db 138 STGVYRSSEHDGTGSPVFAFGVEMATRDIATLEYQWVNNGDAGTGTTRPDNGMLSLGV 197
Qy 186 SYRFQEDAAPVYVAPAPAPAPAVATKHFITLKFNPKATLKPQEGQALDLYTOLSN 245
Db 198 SYRFQEDAAPVYVAPAPAPAVATKHFITLKFNPKATLKPQEGQALDLYTOLSN 257
Qy 246 MIPKDGSAVVLGYTDRIGSEAQNQLSERKASQSVVDLVAKGTPAKTSARGMGESENPTV 305
Db 258 MDPKDGSAVVLGYTDRIGSEAQNQLSERKASQSVVDLVAKGTPAKTSARGMGESENPTV 317
Qy 306 GNTCDNYKARALIDCLAPDRVIEVGYKEVNTQPA 343
Db 318 GNTCDNYKARALIDCLAPDRVIEVGYKEVNTQPA 355
RESULT 2

Result No.	Score	Query Match	Length	DB ID	Description	
1	1712	97.8	356	JC6558	outer membrane pro	
2	15612	84.6	350	S07222	outer membrane pro	
3	15255	83.7	351	1 MMEBAD	outer membrane pro	
4	15111	82.9	346	1 MMEBCA	outer membrane pro	
5	15111	82.9	346	2 A90759	outer membrane pro	
6	15111	82.9	346	2 G85622	outer membrane pro	
7	1439	82.2	350	2 A10626	outer membrane pro	
8	1430	81.7	350	1 MMEBAT	outer membrane pro	
9	1381	5	75.8	S07228	outer membrane pro	
10	1325	5	72.7	353	2 AD0175	probable outer mem
11	1128	5	61.9	238	2 I62385	outer membrane pro
12	1112	5	61.0	244	2 I62333	outer membrane pro
13	1111	60.9	243	2 I62388	outer membrane pro	
14	1110	5	60.9	244	2 I62389	outer membrane pro
15	1109	60.8	243	2 I84511	outer membrane pro	
16	1106	60.7	243	2 I62336	outer membrane pro	
17	1089	59.7	241	2 I62287	outer membrane pro	
18	1084	59.5	241	2 I62391	outer membrane pro	
19	1074	58.9	240	2 I62334	outer membrane pro	
20	1056	5	58.0	238	2 I40703	outer membrane pro
21	646	55	35.5	353	2 C64187	outer membrane pro
22	515	28.3	349	2 B84968	outer membrane pro	
23	443	24.3	321	2 F82104	outer membrane pro	
24	271	14.9	194	2 A45275	21K outer membrane pro	
25	262	14.4	236	2 A27894	outer membrane pro	
26	255	14.0	242	2 C81205	outer membrane pro	
27	251	13.8	240	2 A37004	outer membrane clu	
28	250	13.7	242	2 A81792	outer membrane pro	
29	243	13.3	326	2 S20494	root adhesin - Pse	

S07222 outer membrane protein ompA precursor - Enterobacter aerogenes
 C;Species: Enterobacter aerogenes
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C;Accession: S07222
 R;Braun, G.; Cole, S.T.
 Eur. J. Biochem. 137, 495-500, 1983
 A;Title: Molecular characterization of the gene coding for major outer membrane protein
 A;Reference number: S07222; MUID:84108348; PMID:6363059
 A;Accession: S07222
 A;Molecule type: DNA
 A;Keywords: 1-350 <BRA>
 A;Cross-references: UNIPROT:P09146; UNIPARC:UPI0000130CP1; EMBL:X00254; NID:940837; PIDN
 A;Note: the authors translated the codon CAG for residue 197 as Asn
 C;Genetics:
 A;Gene: ompA
 C;Protein: outer membrane protein A
 C;Keywords: membrane protein
 P;1-21/Domain: signal sequence #status predicted <SIG>
 P;201-212/Domain: outer membrane protein ompA #status predicted <PER>
 P;213-350/Domain: alanine/proline-rich
 P;201-212/Domain: periplasmic #status predicted <PER>
 P;213-350/Domain: periplasmic #status predicted <PER>
 Query Match 84.6% Score 1542; DB 2; Length 350;
 Best Local Similarity 87.5%; Pred. No. 1.8e-10;
 Matches 295; Conservative 10; Mismatches 26; Indels 6; Gaps 2;
 Qy 6 VLNAPKONTWYAGKLGKSYQHDTGTYNGFQNNGPTRNDLGAGAFGGYQVNPyLG 65
 Db 18 VAQAPKONTWYAGGKLGSQHDTGWLNSNLNNNGPTHEOLSGAGAFGGYQVNPyLG 76
 Qy 66 EMGDWLGRMAYKGSVNDGAFRAQGVLTKPQVTAKGIPTRNDLGAGAFGGYQVNPyLG 65
 Db 77 EMGDWLGRMAYKGSVNDGAFRAQGVLTKPQVTAKGIPTRNDLGAGAFGGYQVNPyLG 65
 Qy 126 STGVSRSSEHDTGYSPVFAGGVENAVTRDIASTRLEYQVNNGIDAGTYGTRPNDGMLSLGV 185
 Db 132 SNSIAGDNHDHTGYSPVFAGGVENAVTRDIASTRLEYQVNNGIDAGTYGTRPNDGMLSLGV 191
 Qy 186 SYRGQEDAPVVAAPAPAPEVAKHFLKSDVLFNFKATLKPQEGQALDLYTQSN 245
 Db 192 SYRGQEDAPVVAAPAPAPEVTTKTFLKSDVLFNFKATLKPQEGQALDLYTQSN 251
 Qy 246 MDPKDGSAYVGLGTDRIGSEAYNQLSERKAOQSVVDYLVAKGIPAKGISARGMGESENPT 305
 Db 252 MDPKDGSAYVGLGTDRIGSEAYNQLSERKAOQSVVDYLVAKGIPAKGISARGMGESENPT 311
 Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEYVVTQ 342
 Db 312 GNTCDNVKARAALIDCLAPDRRVAIEVKYKEYVVTQ 348

RESULT 4
 MNCBA
 outer membrane protein A precursor - Escherichia coli (strain K-12)
 N:Alternative names: outer membrane protein II.
 C:Species: Escherichia coli
 C;Date: 30-Sep-1980 #sequence revision 30-Sep-1980 #text change 09-Jul-2004
 C;Accession: A93107; A92862; A92863; A03434
 R;Beck, E.; Bremer, E.
 Nucleic Acids Res. 8, 3011-3024, 1980
 A;Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli
 A;Reference number: A93107; MUID:81053729; PMID:6253901
 A;Accession: A93107
 A;Molecule type: DNA
 A;Residues: 1-346 <BBC>
 A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:V00307; GB:J01654; NID:9146979;
 A;Experimental source: strain K12
 R;Movva, N.R.; Nakamura, K.; Inouye, M.
 J. Mol. Biol. 143, 317-328, 1980
 A;Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli
 A;Reference number: A92862; MUID:8117087; PMID:6260961
 A;Accession: A92862
 A;Molecule type: DNA
 A;Residues: 1-346 <MOV>
 A;Cross-references: UNIPARC:UPI0000130CF0; GB:J01654; GB:V00307; GB:V00358; NID:9146979;
 A;Experimental source: K12, strain K80
 R;Chen, R.; Schmidmayer, W.; Kramer, C.; Chen-Schmidmayer, U.; Henning, U.
 Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
 R;Kuhn, A.; Kiefer, D.; Kohne, C.; Zhu, H.Y.; Techantz, W.R.; Dalbey, R.E.
 Eur. J. Biochem. 226, 891-897, 1994
 A;Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membran
 A;Reference number: S50909; MUID:95112855; PMID:7813480
 A;Accession: S50909
 A;Status: Preliminary
 A;Molecule type: protein

RESULT 3
 MNEBAD
 outer membrane protein A precursor - *Shigella dysenteriae*
 C;Species: *Shigella dysenteriae*
 C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C;Accession: A03435
 R;Braun, G.; Cole, S.T.
 Nucleic Acids Res. 10, 2367-2378, 1982
 A;Title: The nucleotide sequence coding for major outer membrane protein OmpA of *Shigella*
 A;Reference number: A03435; MUID:82221414;
 A;Accession: A03435
 A;Molecule type: DNA
 A;Residues: 1-351 <BRA>
 A;Cross-references: UNIPARC:UPI0000130CPA; GB:V01344; NID:946943; PIDN
 C;Genetics:
 A;Gene: ompA
 C;Protein: outer membrane protein A
 C;Keywords: transmembrane protein
 P;1-21/Domain: signal sequence #status predicted <SIG>
 P;22-351/Domain: outer membrane protein A #status predicted <PER>
 P;22-201/Domain: intramembrane #status predicted <INT>

Db	188	SYRFQGEAAPVVAAPAPAPAEVOTKHTFLKSVDLFNPKNATLKPEGOAALDOLYSQNLN	247	A; Reference number: A03436; MUID: 83287368; PMID: 6349993
Qy	246	MDPKDGSAYVLYGTDIGSEAYNQOLSEKRAQSVDYLVAKGIPAKTSARGMGESENVT	305	A; Accession: A03436 A; Molecule type: DNA A; Residues: 1-350 <FRE>
Db	248	LDPKDGSVYVLYGTDIGSDAYNQGLSERAKSVDYLISKGIPAKTSARGMGESENVT	307	A; Cross-references: UNIPROT: P02936; UNIPARC: UPI0001703A0; GB: X02006; NID: 947798
Qy	306	GNTCDNVKARAALIDCLAPDRVEIEVKYKEYVVTQP	342	C; Genetics:
Db	308	GNTCDNVKRAALIDCLAPDRVEIEVKYKEYVVTQP	344	A; Gene: ompA A; Map position: 20 min A; Function:
	RESULT 7			A; Description: required for the action of colicins and for the stabilization of outer membrane protein A A; Note: cannot serve as the receptor for the ompA-specific phages K3 and Tull
A10626				C; Superfamily: outer membrane protein A C; Keywords: transmembrane protein
				F:1-21/Domain: signal sequence #status predicted <SIG> F:22-359/Product: outer membrane protein A #status predicted <INT> F:22-209/Domain: intramembrane #status predicted <INT> F:200-212/Region: alanine/proline-rich
				F:213-350/Domain: periplasmic #status predicted <PER>
				Query Match 81.7%; Score 1490; DB 1; Length 350; Best Local Similarity 82.8%; Pred. No. 1.66-105; Matches 279; Conservative 24; Mismatches 28; Indels 6; Gaps 2;
				6 VLNAAPKONTWYAGKGKLGISQHDTGFTGQNNGPTRNDLGAGAGGGQVNPNYLGF 65 18 VQAQAPKONTWYAGAKLGMSQYHDTGFI --- HNDGPTPHENQLGAGGQVNPNYVGF 72
				Qy 66 EMGYDWLGRMAYKGSVNDNGAFAKQGVQLTAKLGYPITDDDIYTRLGGRNWRADSKGNYA 125 Db 73 EMGDWLGMRPMYQGDNGDINNGAYKAGQVQLTAKLGYPITDDDIYTRLGGRNWRADTKSNVP 132
				Qy 126 STGVRSRSEHDTGYSVPFAGGVENAVTRDIATRLEYQWNNNIGDAGTVTRPDNGMLSLGV 185 Db 133 G-GPSTKDHDTGYSVPFAGGVEAITPQKHTLKSVDLFNPKNATLKPEGOAALDOLYQTLQSN 245
				Qy 186 SYRFQEDAAPVVAAPAPAPAEVATKHTFLKSVDLFNPKNATLKPEGOAALDOLYQTLQSN 245 Db 192 SYRFQQDAAPVVAAPAPAPAEVATRLEYQWNNNIGDANTIGTRPDNGMLSLGV 191
				Qy 246 MDPRDGASVVLGYTDRIGSEAYNQQLSEKRAQSVDYLVAKGIPAKTSARGMGESENVT 305 Db 252 LDPKDGTSVVLGFIDRISDAYQGLSERAKAQSVDYLTKPSDK1SARGMGESENVT 311
				Qy 306 GNTCDNVKARAALIDCLAPDRVEIEVKYKEYVVTQP 342 Db 312 GNTCDNVKRAALIDCLAPDRVEIEVKYKEYVVTQP 348
				RESULT 9 S07298
				outer membrane protein ompA precursor - <i>Serratia marcescens</i>
				C; Species: <i>Serratia marcescens</i> C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
				C; Accession: S07298 R. Braun, G. i. Cole, S. T. Mol. Gen. Genet. 195, 321-328, 1984 A; Title: DNA sequence analysis of the <i>Serratia marcescens</i> <i>ompA</i> gene: implications
				A; Reference number: S07298; MUID: 6092958 A; Accession: S07298 A; Molecule type: DNA A; Cross-references: UNIPROT: P04845; UNIPARC: UPI0001130CF8; EMBL: X00618; NID: g472
				C; Genetics: A; Gene: ompA C; Superfamily: outer membrane protein A C; Keywords: membrane protein
				F:1-21/Domain: signal sequence #status predicted <SIG> F:22-359/Product: outer membrane protein ompA #status predicted <INT> F:22-209/Domain: intramembrane #status predicted <INT> F:210-212/Region: alanine/proline-rich
				F:220-359/Domain: periplasmic #status predicted <PER>
				Query Match 75.8%; Score 1381.5; DB 2; Length 359
	RESULT 8			MNEBAT
				outer membrane protein A precursor - <i>Salmonella typhimurium</i>
				Alt name: outer membrane major heat-modifiable protein; outer membrane protein
				C; Species: <i>Salmonella typhimurium</i>
				C; Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
				C; Accession: A03436 R. Freudi, R.; Cole, S. T. A; Title: Cloning and molecular characterization of the <i>ompA</i> gene from <i>Salmonella typhimurium</i>
				Query Match 75.8%; Score 1381.5; DB 2; Length 359

Best Local Similarity	78.2%	Pred. No.	2.7e-97;
Matches	269;	Conservative	24;
Mismatches	44;	Indels	7;
Gaps	4;		
Qy	6	VLNAAPKONTWYAGGKLGNQYHDTGFYGNQFQN -NNGPTRNDLGAFFGQYQVNPFYI	63
Db	18	VQAQAPKONTWYAGGKLGSQYHDTGFYGNQFQNIGTHKDLGAGFLGTANQYL	77
		RESULT 11	
	162385	outer membrane protein ompA - Escherichia vulneris (fragment)	
		N;Alternate names: outer membrane protein II	
		C;Species: Escherichia vulneris	
		C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
		R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
		J. Gen. Microbiol. 137, 1911-1921, 1991	
		A;Title: Molecular and evolutionary relationships among enteric bacteria.	
		A;Reference number: 140701; PMID:92065252;	
		A;Accession: 162385	
		A;Status: preliminary; translated from GB/EMBL/DBJ	
		A;Molecule type: DNA	
		A;Residues: 1-218 <RES>	
		A;Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB: M63348; NID:q146984; PIDN: F;98-109/Region: alanine/proline-rich	
		C;Keywords: membrane protein	
		C;Superfamily: outer membrane protein A	
		A;Gene: ompA	
		F;98-109/Region: alanine/proline-rich	
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		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	64	GFEQGYDWLGRMAYKGSVDNGAFAKQGVLQTAKGYPITDDIYTRLGGMWWRADSKGN	123
Db	78	GFEQGYDWLGRMPTKGSVDNGAFAKQGVLQAAKSLPYIADDDIYTRLGGMWWRADSKGN	137
		RESULT 12	
	124	YASTCQVSRSBEHDITGSPVSPVAGGVEWAVTRDIATRLEYQWYNNIGDAGTVTRPQDGMISL	183
Db	138	YGRTCQRLSLSDHDITGSPVSPVLAAGVEYALTKWATRDLQYQFSNIGDAGTVGARPDTMISL	197
Qy	184	GVSYRFQGQD -AAPVAPAPAPAPAPAPATRFLTKSDVLNFENFKATLKPQEGOALDQLYTO	242
Db	198	GVSYRFQGQD -AAPVAPAPVETRFLTKSDVLNFENFKATLKPQEGOALDQLYTO	255
		Query Match	61.9%
		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	243	LSNMDPKDGSAVVGLGVDPITGSEAYNQOLSEKRAQSQVYDYLVAKGIPAKKISARGMGESN	302
Db	256	LSNMDPKDGSVWVGLGVDTAGSDQYQNLSEKRAQSQVYDYLVSKGIPSRSKISARGMGEAD	315
		Query Match	61.9%
		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	303	PVQNTCDVKA -A-LIDCLAPDRRVEIUVKGKREVNTQPVAG	344
Db	316	AVQNTCDVKA -GKSGRATKAQ1QVCLAPDRRVEIUVKG1KDVTQPGQ	359
		Query Match	61.9%
		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	304	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	313	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	351
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		Best Local Similarity	90.1%
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		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	305	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	312	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Best Local Similarity	90.1%
		Matches	219;
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		Mismatches	12;
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		Gaps	1;
Qy	306	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	311	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	351
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		Gaps	1;
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		Best Local Similarity	90.1%
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		Conservative	7;
		Mismatches	12;
		Indels	5;
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Db	309	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
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		Gaps	1;
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Db	307	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Mismatches	12;
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		Conservative	7;
		Mismatches	12;
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		Matches	219;
		Conservative	7;
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Qy	314	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	303	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	315	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	302	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	316	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	301	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Best Local Similarity	90.1%
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		Conservative	7;
		Mismatches	12;
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Db	300	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
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Db	299	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
		Query Match	61.9%
		Best Local Similarity	90.1%
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		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	319	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	298	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
		Query Match	61.9%
		Best Local Similarity	90.1%
		Matches	219;
		Conservative	7;
		Mismatches	12;
		Indels	5;
		Gaps	1;
Qy	320	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	297	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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Qy	321	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	296	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Indels	5;
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Qy	322	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	295	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Mismatches	12;
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		Gaps	1;
Qy	323	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	294	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Mismatches	12;
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		Gaps	1;
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		Mismatches	12;
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		Mismatches	12;
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		Gaps	1;
Qy	326	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
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		Conservative	7;
		Mismatches	12;
		Indels	5;
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Qy	327	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
Db	290	VGNTCDVKA -LIDCLAPDRRVEIUVKGKREVNTQPVAG	350
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		Indels	5;
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		Matches	219;
		Conservative	7;
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Qy	330	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
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		Conservative	7;
		Mismatches	12;
		Indels	5;
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		Matches	219;
		Conservative	7;
		Mismatches	12;
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Qy	332	VGNTCDVKA -AALIDCLAPDRRVEIUVKGKREVNTQPVAG	342
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		Mismatches	12;
		Indels	5;
		Gaps	1;</td

C;Keywords: membrane protein
F:104-115/Region: alanine/proline-rich

Query Match 61.0%; Score 1112.5; DB 2; Length 244;
Best Local Similarity 87.2%; Pred. No. 4.2e-77;
Matches 212; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

Qy 93 LTAKLGYPTDDIYTRIGGMWRAKGNVASTGVSPEHDGTGVSPFAGGVENAVTR 152
Db 1 LTAKLGYPTDDIYTRIGGMWRAKGNVASTGVSPEHDGTGVSPFAGGVENAVTR 152

Qy 162389 I62389 RESULT 14
Db 61 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 211
C;Species: Escherichia vulneris (ATCC 33821) (fragment)

Qy 212 HFTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRISSEAYNQQL 271
Db 121 HFTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRISSEAYNQQL 180

Qy 272 SERKRAQSVDYLVAKGIPAKKISARGMGEESNPVGTNTCDNVKARAALIDCLAPDRVEI 331
Db 181 SERKRAQSVDYLVAKGIPAKKISARGMGEESNPVGTNTCDNVKARAALIDCLAPDRVEI 240

332 VKG 334
Db 241 VKG 243

Qy 162388 I62388 RESULT 15
Db 61 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 211
C;Species: Escherichia fergusonii (ATCC 35472) (fragment)

Qy 162389 I62389 RESULT 15
Db 121 HFTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRISSEAYNQQL 271
C;Species: Escherichia fergusonii (ATCC 35469) (fragment)

Qy 93 LTAKLGYPTDDIYTRIGGMWRAKGNVASTGVSPEHDGTGVSPFAGGVENAVTR 152
Db 121 HFTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRISSEAYNQQL 180

Qy 153 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 211
Db 61 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 211
C;Cross-references: UNIPROT:R24747; UNIPARC:UPI0000130CF3; GB:M63352; PIDN:9146990; PIDN:140701; MUID:92065252; PMID:1955870

A;Gene: ompA
A;Experimental source: ATCC 35472
A;Accession: 162389
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:R24747; UNIPARC:UPI0000130CF3; GB:M63352; PIDN:9146990; PIDN:140701; MUID:92065252; PMID:1955870

A;Gene: ompA
A;Experimental source: ATCC 35472
A;Accession: 162389
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
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A;Gene: ompA
A;Experimental source: ATCC 35472
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Qy 93 LTAKLGYPTDDIYTRIGGMWRAKGNVASTGVSPEHDGTGVSPFAGGVENAVTR 152
Db 1 LTAKLGYPTDDIYTRIGGMWRAKGNVASTGVSPEHDGTGVSPFAGGVENAVTR 152

Qy 153 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 212
Db 61 DIATRLEYQWNNGIDTGTTRPDNGMISLGYSYRFQ-QEDAAPVWAPAPAPEVATK 212

Qy 213 FTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRIGSPEAYNQQL 272
Db 121 FTLKSVDLNFNKATLKEPGQALDQLYTQLSNMPKDGSAVVLGYTRIGSPEAYNQQL 180

A: Molecule type: DNA
A: Residues: 1-243 <RES>
A: Cross-references: UNIPROT:P24747; UNIPARC:UPI000016F6FB; GB:M63351; NID:9146982; PIDN:
A: Experimental source: ATCC 35469
C: Genetics:
A: Gene: *ompA*
C: Superfamily: outer membrane protein A
C: Keywords: membrane protein
F: 1.03-114/Region: alanine/proline-rich

Query Match 60.8%; Score 1109; DB 2; Length 243;
Best Local Similarity 87.2%; Pred. No. 7; 78-77;
Matches 211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 93 LTAKLGYPTDDDIYTRIGGMWYRADSKGNYASTGVSRSEHDTGVSPVFAAGGVEAWTR 152
1 LTAKLGYPTDDDIYTRIGGMWYRADSKGNYASTGVSRSEHDTGVSPVFAAGGVEAWTR 60

Qy 153 DIATRLEYCQWNNIGDAGTVGTRPDNGMISLGCVSYRFQEDAAAPVVAAPAPAPEVATKH 212
Db 61 EIAATRLEYCQWNNIGDANTIGTREDNGLISLGCVSYRFQGEAAPVVAAPAPAPEVCKH 120

Qy 213 FTLKSDVLFENKATLKEPQQALDQLYTQLSNDPDKGSAAVVLGYTDIGSAYNQQLS 272
Db 121 FTLKSDVLFENKATLKEPQQALDQLYSQLSNDPDKGSAAVVLGYTDIGSAYNQQLS 180

Qy 273 ERRAQSVVVDYLVAKGIPACKKISARGMGESENPTGNTCDNVKARAALIDCLAPDRRVEV 332
Db 181 ERRAQSVVVDYLISKGIPACKKISARGMGESENPTGNTCDNVKARAALIDCLAPDRRVEV 240

Qy 333 KG 334
Db 241 KG 242

Search completed: November 26, 2005, 00:10:29
Job time : 42 secs

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